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OM protein - protein search, using sw model

Run on: December 2, 2003, 02:15:49 ; Search time 218.096 Seconds
(without alignments)
246.943 Million cell updates/sec

Title: US-09-607-745-9

Perfect score: 1600

Sequence: 1 MDSKGSQKSRLLLLVSN.....LNWIYVWKAELSRHHHHH 292

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1266	79.1	406	9	US-09-851-588-6
2	1266	79.1	423	11	US-09-776-191-72
3	1266	79.1	423	15	US-10-264-820-23
4	1266	79.1	423	15	US-10-254-289-2
5	1266	79.1	432	11	US-09-888-257A-7
6	1266	79.1	432	11	US-09-945-374-275
7	1266	79.1	432	12	US-10-015-387A-275
8	1266	79.1	432	12	US-10-063-735-112
9	1266	79.1	432	12	US-10-006-130A-275
10	1266	79.1	432	12	US-10-199-672-330
11	1266	79.1	432	12	US-10-006-172A-275
12	1266	79.1	432	12	US-10-187-749-330
13	1266	79.1	432	12	US-10-194-457-330
14	1266	79.1	432	12	US-10-184-642-330
15	1266	79.1	432	12	US-10-196-747-330
Sequence 6, Appli					
Sequence 72, Appl					
Sequence 23, Appl					
Sequence 2, Appli					
Sequence 7, Appli					
Sequence 275, App					
Sequence 275, App					
Sequence 112, App					
Sequence 275, App					
Sequence 330, App					
Sequence 275, App					
Sequence 330, App					
Sequence 330, App					
Sequence 330, App					

16	1266	79.1	432	12	US-10-015-332A-275	Sequence 275, App
17	1266	79.1	432	12	US-10-017-253A-275	Sequence 275, App
18	1266	79.1	432	12	US-10-173-689-330	Sequence 330, App
19	1266	79.1	432	12	US-10-173-690-330	Sequence 330, App
20	1266	79.1	432	12	US-10-173-691-330	Sequence 330, App
21	1266	79.1	432	12	US-10-173-692-330	Sequence 330, App
22	1266	79.1	432	12	US-10-173-693-330	Sequence 330, App
23	1266	79.1	432	12	US-10-173-694-330	Sequence 330, App
24	1266	79.1	432	12	US-10-173-698-330	Sequence 330, App
25	1266	79.1	432	12	US-10-173-699-330	Sequence 330, App
26	1266	79.1	432	12	US-10-174-569-330	Sequence 330, App
27	1266	79.1	432	12	US-10-174-583-330	Sequence 330, App
28	1266	79.1	432	12	US-10-174-587-330	Sequence 330, App
29	1266	79.1	432	12	US-10-174-589-330	Sequence 330, App
30	1266	79.1	432	12	US-10-174-591-330	Sequence 330, App
31	1266	79.1	432	12	US-10-175-736-330	Sequence 330, App
32	1266	79.1	432	12	US-10-175-742-330	Sequence 330, App
33	1266	79.1	432	12	US-10-175-744-330	Sequence 330, App
34	1266	79.1	432	12	US-10-175-745-330	Sequence 330, App
35	1266	79.1	432	12	US-10-175-748-330	Sequence 330, App
36	1266	79.1	432	12	US-10-175-751-330	Sequence 330, App
37	1266	79.1	432	12	US-10-175-754-330	Sequence 330, App
38	1266	79.1	432	12	US-10-176-480-330	Sequence 330, App
39	1266	79.1	432	12	US-10-176-489-330	Sequence 330, App
40	1266	79.1	432	12	US-10-176-754-330	Sequence 330, App
41	1266	79.1	432	12	US-10-176-755-330	Sequence 330, App
42	1266	79.1	432	12	US-10-176-759-330	Sequence 330, App
43	1266	79.1	432	12	US-10-176-920-330	Sequence 330, App
44	1266	79.1	432	12	US-10-176-922-330	Sequence 330, App
45	1266	79.1	432	12	US-10-176-924-330	Sequence 330, App

ALIGNMENTS

RESULT 1
US-09-851-588-6
; Sequence 6, Application US/09851588
; Patent No. US20020042067A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt C.
; APPLICANT: Wilson, Keith E.
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AN
; FILE REFERENCE: A-68829-1/DJBE/JUD/AMS
; CURRENT APPLICATION NUMBER: US/09/851.588
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/642,252
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: US 09/656,002
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-851-588-6

Query Match		79.1%	Score 1266;	DB 9;	Length 406;
Best Local Similarity		97.4%	Pred. No. 5.9e-117;		
Matches 228;		Conservative 2;	Mismatches 4;	Indels 0;	Gaps 0;
QY	51	KIVGGYALDVDSWPMQVSIQYDKQHVCGSILDPHWLTAACFRKHTDVFNNKVRAGSD	110		
Db	173	RVVGGEEASVDVSWPMQVSIQYDKQHVCGSILDPHWLTAACFRKHTDVFNNKVRAGSD	232		
QY	111	KLGGFPLSLAVAKIIIIIFBNPMYPKNDIALMKLOPFTFSGTVPICLPFFDEELTPATP	170		
Db	233	KLGGFPLSLAVAKIIIIIFBNPMYPKNDIALMKLOPFTFSGTVPICLPFFDEELTPATP	292		
QY	171	LWIIGWGTQNGKMSDILLOASVQVDSIDTRCNADDAAYQGEVTEKMCACIGPEGVDTC	230		

Db 293 LWTIGGFTKQNGKMSDILQASVQVIDSTRCNADDAYQCGEVTCKMCAIGPEGGYDTC 352
QY 231 QGDSGGPLMTQSDQHWVGVISWGYCGGPGSTPGVYTKVSAYLNWIYVWKAEL 284
Db 353 QGDSGGPLMTQSDQHWVGVISWGYCGGPGSTPGVYTKVSAYLNWIYVWKAEL 406

RESULT 2

US-09-776-191-72
; Sequence 72, Application US/09776191
; Publication No. US20030119168A1
; GENERAL INFORMATION:
; APPLICANT: Edwin L. Madison
; APPLICANT: Edgar O. Ong
; APPLICANT: Giann-Chern Yeh
; APPLICANT: Corvas International, Inc.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: TRANSMEMBRANE SERINE PROTEASES, THE ENCODED PROTEINS AND
; TITLE OF INVENTION: METHODS BASED THEREON
; FILE REFERENCE: 24745-1607
; CURRENT APPLICATION NUMBER: US/09/776,191
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,124
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/234,840
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/179,982
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 60/183,542
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: 09/657,968
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-776-191-72

Query Match 79.1%; Score 1266; DB 11; Length 423;
Best Local Similarity 97.4%; Pred. No. 6.2e-117;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 51 KIVGGYALVDSDWPMQVSIQYDKQHVCGSILDPHWLTAHCFRKHDTVFNWKAEL 110
Db 190 RVVGGEEASVDSWPMQVSIQYDKQHVCGSILDPHWLTAHCFRKHDTVFNWKAEL 249
QY 111 KLGSPFLAVAKIIIEFNPMYKNDIALMKLQFPLTFSGTVRPICLPFFDELTPTATP 170
Db 250 KLGSPFLAVAKIIIEFNPMYKNDIALMKLQFPLTFSGTVRPICLPFFDELTPTATP 309
QY 171 LWTIGWFTKQNGKMSDILQASVQVIDSTRCNADDAYQCGEVTCKMCAIGPEGGYDTC 230
Db 310 LWTIGWFTKQNGKMSDILQASVQVIDSTRCNADDAYQCGEVTCKMCAIGPEGGYDTC 369
QY 231 QGDSGGPLMTQSDQHWVGVISWGYCGGPGSTPGVYTKVSAYLNWIYVWKAEL 284
Db 370 QGDSGGPLMTQSDQHWVGVISWGYCGGPGSTPGVYTKVSAYLNWIYVWKAEL 423

RESULT 3

US-10-264-820-23
; Sequence 23, Application US/10264820
; Publication No. US20030108926A1
; GENERAL INFORMATION:
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030108926A1 Methods of Diagnosing Colorectal Cancer,
; TITLE OF INVENTION: Compositions, and Methods of Screening for Colorectal
; TITLE OF INVENTION: Cancer Modulators
; FILE REFERENCE: 018501-006141US
; CURRENT APPLICATION NUMBER: US/10/264,820

; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/268,866
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: US 09/435,945
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/436,983
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/450,857
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: US 09/453,850
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 09/493,444
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 09/525,993
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human CGAS
US-10-264-820-23

Query Match 79.1%; Score 1266; DB 15; Length 423;
Best Local Similarity 97.4%; Pred. No. 6.2e-117;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 51 KIVGGYALVDSDWPMQVSIQYDKQHVCGSILDPHWLTAHCFRKHDTVFNWKAEL 110
Db 190 RVVGGEEASVDSWPMQVSIQYDKQHVCGSILDPHWLTAHCFRKHDTVFNWKAEL 249
QY 111 KLGSPFLAVAKIIIEFNPMYKNDIALMKLQFPLTFSGTVRPICLPFFDELTPTATP 170
Db 250 KLGSPFLAVAKIIIEFNPMYKNDIALMKLQFPLTFSGTVRPICLPFFDELTPTATP 309
QY 171 LWTIGWFTKQNGKMSDILQASVQVIDSTRCNADDAYQCGEVTCKMCAIGPEGGYDTC 230
Db 310 LWTIGWFTKQNGKMSDILQASVQVIDSTRCNADDAYQCGEVTCKMCAIGPEGGYDTC 369
QY 231 QGDSGGPLMTQSDQHWVGVISWGYCGGPGSTPGVYTKVSAYLNWIYVWKAEL 284
Db 370 QGDSGGPLMTQSDQHWVGVISWGYCGGPGSTPGVYTKVSAYLNWIYVWKAEL 423

RESULT 4

US-10-254-289-2
; Sequence 2, Application US/10254289
; Publication No. US20030118509A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AN
; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-69108/DJB/JUD/AMS
; CURRENT APPLICATION NUMBER: US/10/254,289
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US/09/656,002
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/525,993
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 09/493,444
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US 00/07044
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-254-289-2

Query Match 79.1%; Score 1266; DB 15; Length 423;
Best Local Similarity 97.4%; Pred. No. 6.2e-117;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 51 KIVGGYALDVSFQVSIQYDKQHVCGSILDPHWLTAHCFRKHDTVFNKVRAGSD 110
Db 190 RVVGGEEASVDSFQVSIQYDKQHVCGSILDPHWLTAHCFRKHDTVFNKVRAGSD 249
QY 111 KLGSPFLSAVAKIIIEFNPMYPKNDIALMKLOPFTFSGTVRPICLPFFDEELTPATP 170
Db 250 KLGSPFLSAVAKIIIEFNPMYPKNDIALMKLOPFTFSGTVRPICLPFFDEELTPATP 309
QY 171 LWTIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMCAGIPEGGVDTTC 230
Db 310 LWTIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMCAGIPEGGVDTTC 369
QY 231 QGDSGGFLMYQSDQHVGVSVGCGGPGSTPGVYTKVSAYLNWIYNVWKAE 284
Db 370 QGDSGGFLMYQSDQHVGVSVGCGGPGSTPGVYTKVSAYLNWIYNVWKAE 423

RESULT 5

US-09-888-257A-7
; Sequence 7, Application US/09888257A
; Publication No. US2003060612A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Polakis, Paul
; APPLICANT: Smith, Victoria
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5002R1
; CURRENT APPLICATION NUMBER: US/09/888,257A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/063,540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: US 60/089,653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/099,792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/103,678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: US 60/235,451
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 7
; LENGTH: 432

; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-888-257A-7

Query Match 79.1%; Score 1266; DB 11; Length 432;
Best Local Similarity 97.4%; Pred. No. 6.3e-117;
Matches 238; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 51 KIVGGYALDVSFQVSIQYDKQHVCGSILDPHWLTAHCFRKHDTVFNKVRAGSD 110
Db 199 RVVGGEEASVDSFQVSIQYDKQHVCGSILDPHWLTAHCFRKHDTVFNKVRAGSD 258
QY 111 KLGSPFLSAVAKIIIEFNPMYPKNDIALMKLOPFTFSGTVRPICLPFFDEELTPATP 170
Db 259 KLGSPFLSAVAKIIIEFNPMYPKNDIALMKLOPFTFSGTVRPICLPFFDEELTPATP 318
QY 171 LWTIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMCAGIPEGGVDTTC 230
Db 319 LWTIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMCAGIPEGGVDTTC 378
QY 231 QGDSGGFLMYQSDQHVGVSVGCGGPGSTPGVYTKVSAYLNWIYNVWKAE 284
Db 379 QGDSGGFLMYQSDQHVGVSVGCGGPGSTPGVYTKVSAYLNWIYNVWKAE 432

RESULT 6

US-09-946-374-275
; Sequence 275, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596

1

;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105266
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807

Query Match 79.1%; Score 1266; DB 11; Length 432;
Best Local Similarity 97.4%; Pred. No. 6.3e-117;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 51 KIVGGYALVDSPWQVSIQYDKQHVCGGSLDHPHWLTAHCFRKHDTVFNWVKRAGSD 110
Db :|||||
QY 199 RVVGEASVDSWPWQVSIQYDKQHVCGGSLDHPHWLTAHCFRKHDTVFNWVKRAGSD 258
Db :|||||
QY 111 KLSFPLSLAVAKIIIEFNPMYPKNDIALMKLOPFTFSGTVRPICLPFFDEELTPATP 170
Db :|||||
QY 259 KLSFPLSLAVAKIIIEFNPMYPKNDIALMKLOPFTFSGTVRPICLPFFDEELTPATP 318
QY 171 LWTIGWFTKQNGKMSDILLQASQVVIDSTRCNADDAYQGEVTEKMKCAGIPEGGVDTTC 230
Db :|||||
QY 319 LWTIGWFTKQNGKMSDILLQASQVVIDSTRCNADDAYQGEVTEKMKCAGIPEGGVDTTC 378
QY 231 QGDSGGPLMYQSDQWVHVGVSVWGYGCGGPGSTPGVYTKVSAYLNWIYVWKAEL 284
Db :|||||
QY 379 QGDSGGPLMYQSDQWVHVGVSVWGYGCGGPGSTPGVYTKVSAYLNWIYVWKAEL 432

RESULT 7

US-10-015-387A-275
; Sequence 275, Application US/10015387A
; Publication No. US20030135034A1

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 275
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-015-387A-275

Query Match 79.1%; Score 1266; DB 12; Length 432;
Best Local Similarity 97.4%; Pred. No. 6.3e-117;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 51 KIVGGYALVDSPWQVSIQYDKQHVCGGSLDHPHWLTAHCFRKHDTVFNWVKRAGSD 110
Db :|||||
QY 199 RVVGEASVDSWPWQVSIQYDKQHVCGGSLDHPHWLTAHCFRKHDTVFNWVKRAGSD 258
Db :|||||
QY 111 KLSFPLSLAVAKIIIEFNPMYPKNDIALMKLOPFTFSGTVRPICLPFFDEELTPATP 170
Db :|||||
QY 259 KLSFPLSLAVAKIIIEFNPMYPKNDIALMKLOPFTFSGTVRPICLPFFDEELTPATP 318

QY 171 LWTIGWFTKQNGKMSDILLQASQVVIDSTRCNADDAYQGEVTEKMKCAGIPEGGVDTTC 230
Db :|||||
QY 319 LWTIGWFTKQNGKMSDILLQASQVVIDSTRCNADDAYQGEVTEKMKCAGIPEGGVDTTC 378
QY 231 QGDSGGPLMYQSDQWVHVGVSVWGYGCGGPGSTPGVYTKVSAYLNWIYVWKAEL 284
Db :|||||
QY 379 QGDSGGPLMYQSDQWVHVGVSVWGYGCGGPGSTPGVYTKVSAYLNWIYVWKAEL 432

RESULT 8

US-10-063-735-112
; Sequence 112, Application US/10063735
; Publication No. US20030138882A1

; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,735
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170

; SEQ ID NO 112
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-063-735-112

Query Match 79.1%; Score 1266; DB 12; Length 432;

Best Local Similarity 97.4%; Pred. No. 6.3e-117;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 51 KIVGGYALVDSPWQVSIQYDKQHVCGGSLDHPHWLTAHCFRKHDTVFNWVKRAGSD 110
Db :|||||
QY 199 RVVGEASVDSWPWQVSIQYDKQHVCGGSLDHPHWLTAHCFRKHDTVFNWVKRAGSD 258
Db :|||||
QY 111 KLSFPLSLAVAKIIIEFNPMYPKNDIALMKLOPFTFSGTVRPICLPFFDEELTPATP 170
Db :|||||
QY 259 KLSFPLSLAVAKIIIEFNPMYPKNDIALMKLOPFTFSGTVRPICLPFFDEELTPATP 318
QY 171 LWTIGWFTKQNGKMSDILLQASQVVIDSTRCNADDAYQGEVTEKMKCAGIPEGGVDTTC 230
Db :|||||
QY 319 LWTIGWFTKQNGKMSDILLQASQVVIDSTRCNADDAYQGEVTEKMKCAGIPEGGVDTTC 378
QY 231 QGDSGGPLMYQSDQWVHVGVSVWGYGCGGPGSTPGVYTKVSAYLNWIYVWKAEL 284
Db :|||||
QY 379 QGDSGGPLMYQSDQWVHVGVSVWGYGCGGPGSTPGVYTKVSAYLNWIYVWKAEL 432

RESULT 9

US-10-006-130A-275

; Sequence 275, Application US/10006130A
; Publication No. US20030148375A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

```
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 275
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-130A-275

Query Match          79.1%; Score 1266; DB 12; Length 432;
Best Local Similarity 97.4%; Pred. No. 6.3e-117;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 51 KIVGYALDVSWPQVSIQYDKQHVCGSILDPHWLTAACHCFKHTDVFNWVKRAGSD 110
    :|||
Db 199 RVVGEASVDSWPQVSIQYDKQHVCGSILDPHWLTAACHCFKHTDVFNWVKRAGSD 258

Qy 111 KLGSPPSLAVALKIIIEFNPMYPKNDIALMKLOPPLTFSGTVRPICLPFFDEELTPATP 170
    :|||
Db 259 KLGSPPSLAVALKIIIEFNPMYPKNDIALMKLOPPLTFSGTVRPICLPFFDEELTPATP 318

Qy 171 LWIIGWFTKQGGKMSDILLQASVQVIDSTRCNADDAVQGEVTEKMCAGIPGGVDTC 230
    :|||
Db 319 LWIIGWFTKQGGKMSDILLQASVQVIDSTRCNADDAVQGEVTEKMCAGIPGGVDTC 378

Qy 231 QDSSGGLMYQSDQWHVGVISWGYCGGSPSTPGVYTKVSAYLNIYNNWKAEL 284
    :|||
Db 379 QDSSGGLMYQSDQWHVGVISWGYCGGSPSTPGVYTKVSAYLNIYNNWKAEL 432

RESULT 10
US-10-199-672-330
; Sequence 330, Application US/10199672
; Publication No. US20030148442A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/199,672
; CURRENT FILING DATE: 2002-07-18
; Prior Application Number: US/10/052,586
; Prior Filing Date: 2002-01-15
; Prior Application Number: 60/059263
; Prior Filing Date: 1997-09-18
; Prior Application Number: 60/059266
; Prior Filing Date: 1997-09-18
; Prior Application Number: 60/062250
; Prior Filing Date: 1997-10-17
; Prior Application Number: 60/063120
; Prior Filing Date: 1997-10-24
; Prior Application Number: 60/063121
; Prior Filing Date: 1997-10-24
; Prior Application Number: 60/063486
; Prior Filing Date: 1997-10-21
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; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-672-330

Query Match          79.1%; Score 1266; DB 12; Length 432;
Best Local Similarity 97.4%; Pred. No. 6.3e-117;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 51 KIVGYALDVSWPQVSIQYDKQHVCGSILDPHWLTAACHCFKHTDVFNWVKRAGSD 110
    :|||
Db 199 RVVGEASVDSWPQVSIQYDKQHVCGSILDPHWLTAACHCFKHTDVFNWVKRAGSD 258

Qy 111 KLGSPPSLAVALKIIIEFNPMYPKNDIALMKLOPPLTFSGTVRPICLPFFDEELTPATP 170
    :|||
Db 259 KLGSPPSLAVALKIIIEFNPMYPKNDIALMKLOPPLTFSGTVRPICLPFFDEELTPATP 318

Qy 171 LWIIGWFTKQGGKMSDILLQASVQVIDSTRCNADDAVQGEVTEKMCAGIPGGVDTC 230
    :|||
Db 319 LWIIGWFTKQGGKMSDILLQASVQVIDSTRCNADDAVQGEVTEKMCAGIPGGVDTC 378

Qy 231 QDSSGGLMYQSDQWHVGVISWGYCGGSPSTPGVYTKVSAYLNIYNNWKAEL 284
    :|||
Db 379 QDSSGGLMYQSDQWHVGVISWGYCGGSPSTPGVYTKVSAYLNIYNNWKAEL 432

RESULT 11
US-10-006-172A-275
; Sequence 275, Application US/10006172A
; Publication No. US20030153000A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C11
; CURRENT APPLICATION NUMBER: US/10/006,172A
; CURRENT FILING DATE: 2002-03-19
; Prior Application Number: 60/098716
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098723
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098749
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098750
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098803
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/098821
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/098843
; Prior Filing Date: 1998-09-02
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1	PRIOR FILING DATE: 1998-09-23	
2	PRIOR APPLICATION NUMBER: 60/101476	
3	PRIOR FILING DATE: 1998-09-23	
4	PRIOR APPLICATION NUMBER: 60/101477	
5	PRIOR FILING DATE: 1998-09-23	
6	PRIOR APPLICATION NUMBER: 60/101479	
7	PRIOR FILING DATE: 1998-09-23	
8	PRIOR APPLICATION NUMBER: 60/101738	
9	PRIOR FILING DATE: 1998-09-24	
10	PRIOR APPLICATION NUMBER: 60/101741	
11	PRIOR FILING DATE: 1998-09-24	
12	PRIOR APPLICATION NUMBER: 60/101743	
13	PRIOR FILING DATE: 1998-09-24	
14	PRIOR APPLICATION NUMBER: 60/101915	
15	PRIOR FILING DATE: 1998-09-24	
16	PRIOR APPLICATION NUMBER: 60/101916	
17	PRIOR FILING DATE: 1998-09-24	
18	PRIOR APPLICATION NUMBER: 60/102207	
19	PRIOR FILING DATE: 1998-09-29	
20	PRIOR APPLICATION NUMBER: 60/102240	
21	PRIOR FILING DATE: 1998-09-29	
22	PRIOR APPLICATION NUMBER: 60/102307	
23	PRIOR FILING DATE: 1998-09-29	
24	PRIOR APPLICATION NUMBER: 60/102330	
25	PRIOR FILING DATE: 1998-09-29	
26	PRIOR APPLICATION NUMBER: 60/102331	
27	PRIOR FILING DATE: 1998-09-29	
28	PRIOR APPLICATION NUMBER: 60/102484	
29	PRIOR FILING DATE: 1998-09-30	
30	PRIOR APPLICATION NUMBER: 60/102487	
31	PRIOR FILING DATE: 1998-09-30	
32	PRIOR APPLICATION NUMBER: 60/102570	
33	PRIOR FILING DATE: 1998-09-30	
34	PRIOR APPLICATION NUMBER: 60/102571	
35	PRIOR FILING DATE: 1998-09-30	
36	PRIOR APPLICATION NUMBER: 60/102684	
37	PRIOR FILING DATE: 1998-10-01	
38	PRIOR APPLICATION NUMBER: 60/102687	
39	PRIOR FILING DATE: 1998-10-01	
40	PRIOR APPLICATION NUMBER: 60/102965	
41	PRIOR FILING DATE: 1998-10-02	
42	PRIOR APPLICATION NUMBER: 60/103258	
43	PRIOR FILING DATE: 1998-10-06	
44	PRIOR APPLICATION NUMBER: 60/103258	
45	PRIOR FILING DATE: 1998-10-06	
46	PRIOR APPLICATION NUMBER: 60/103314	
47	PRIOR FILING DATE: 1998-10-07	
48	PRIOR APPLICATION NUMBER: 60/103315	
49	PRIOR FILING DATE: 1998-10-07	
50	PRIOR APPLICATION NUMBER: 60/103328	
51	PRIOR FILING DATE: 1998-10-07	
52	PRIOR APPLICATION NUMBER: 60/103395	
53	PRIOR FILING DATE: 1998-10-07	
54	PRIOR APPLICATION NUMBER: 60/103396	
55	PRIOR FILING DATE: 1998-10-07	
56	PRIOR APPLICATION NUMBER: 60/103401	
57	PRIOR FILING DATE: 1998-10-07	
58	PRIOR APPLICATION NUMBER: 60/103449	
59	PRIOR FILING DATE: 1998-10-06	
60	PRIOR APPLICATION NUMBER: 60/103633	
61	PRIOR FILING DATE: 1998-10-08	
62	PRIOR APPLICATION NUMBER: 60/103678	
63	PRIOR FILING DATE: 1998-10-08	
64	PRIOR APPLICATION NUMBER: 60/103679	
65	PRIOR FILING DATE: 1998-10-08	
66	PRIOR APPLICATION NUMBER: 60/103711	
67	PRIOR FILING DATE: 1998-10-08	
68	PRIOR APPLICATION NUMBER: 60/104257	
69	PRIOR FILING DATE: 1998-10-14	
70	PRIOR APPLICATION NUMBER: 60/104987	
71	PRIOR FILING DATE: 1998-10-20	
72	PRIOR APPLICATION NUMBER: 60/105000	
73	PRIOR FILING DATE: 1998-10-20	
74	PRIOR APPLICATION NUMBER: 60/105002	
75	PRIOR FILING DATE: 1998-10-20	

; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 79.1%; Score 1266; DB 12; Length 432;
Best Local Similarity 97.4%; Pred. No. 6.3e-117;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 51 KIVGYALDVDSWPQVSIQYDKQHVCGSILDPHWLTAACHCRKHTDVFNWVKVAGSD 110
Db 199 RVUGGEASVDSWPQVSIQYDKQHVCGSILDPHWLTAACHCRKHTDVFNWVKVAGSD 258

Qy 111 KLGSPPLSAVAKIIIEFNPMYPKNDIALMKLOPLTFSGTVRPICLPFFDEELTPATP 170
Db 259 KLGSPPLSAVAKIIIEFNPMYPKNDIALMKLOPLTFSGTVRPICLPFFDEELTPATP 318

Qy 171 LWIIGWGTQKNGKMSDILLQASVQVIDSTRCNADDDAYQGEVTEKMCAGIPEGGVDT 230
Db 319 LWIIGWGTQKNGKMSDILLQASVQVIDSTRCNADDDAYQGEVTEKMCAGIPEGGVDT 378

Qy 231 QGDSGGPLMYQSDQHVHVGVISWGYGCGPSTPGVYTKVSAYLNWIYNWKAEL 284
Db 379 QGDSGGPLMYQSDQHVHVGVISWGYGCGPSTPGVYTKVSAYLNWIYNWKAEL 432

RESULT 12
US-10-187-749-330
; Sequence 330, Application US/10187749
; Publication No. US20030153036A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/187,749
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-187-749-330

Query Match 79.1%; Score 1266; DB 12; Length 432;
Best Local Similarity 97.4%; Pred. No. 6.3e-117;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 51 KIVGYALDVDSWPQVSIQYDKQHVCGSILDPHWLTAACHCRKHTDVFNWVKVAGSD 110
Db 199 RVUGGEASVDSWPQVSIQYDKQHVCGSILDPHWLTAACHCRKHTDVFNWVKVAGSD 258

Qy 111 KLGSPPLSAVAKIIIEFNPMYPKNDIALMKLOPLTFSGTVRPICLPFFDEELTPATP 170
Db 259 KLGSPPLSAVAKIIIEFNPMYPKNDIALMKLOPLTFSGTVRPICLPFFDEELTPATP 318

Qy 171 LWIIGWGTQKNGKMSDILLQASVQVIDSTRCNADDDAYQGEVTEKMCAGIPEGGVDT 230
Db 319 LWIIGWGTQKNGKMSDILLQASVQVIDSTRCNADDDAYQGEVTEKMCAGIPEGGVDT 378

Qy 231 QGDSGGPLMYQSDQHVHVGVISWGYGCGPSTPGVYTKVSAYLNWIYNWKAEL 284
Db 379 QGDSGGPLMYQSDQHVHVGVISWGYGCGPSTPGVYTKVSAYLNWIYNWKAEL 432

RESULT 13
US-10-194-457-330
; Sequence 330, Application US/10194457
; Publication No. US20030153037A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C296
; CURRENT APPLICATION NUMBER: US/10/194,457
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540


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/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063541
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063544
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 330
/ LENGTH: 432
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-194-457-330

Query Match          79.1%; Score 1266; DB 12; Length 432;
Best Local Similarity 97.4%; Pred. No. 6.3e-117;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 51 KIVGGYALVDSPWQVSIQYDKQHVCGSILDPHWLTAHCFRKHTDVFNNKVRAGSD 110
Db 199 RVVGGEEASVDSWPQVSIQYDKQHVCGSILDPHWLTAHCFRKHTDVFNNKVRAGSD 258

QY 111 KLGSPFLAVAKIIIEFNPMYPKNDIALMKLOFPLTFSGTVPICLPFFDEELTPATP 170
Db 259 KLGSPFLAVAKIIIEFNPMYPKNDIALMKLOFPLTFSGTVPICLPFFDEELTPATP 318

QY 171 LWTIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAVQGEVTEKMKCAGIPEGGVDTTC 230
Db 319 LWTIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAVQGEVTEKMKCAGIPEGGVDTTC 378

QY 231 QGDSGGPLMYQSDQHWVGVISWGYCGGSPSTFGVYTKVSAYLNWYNNWKAEK 284
Db 379 QGDSGGPLMYQSDQHWVGVISWGYCGGSPSTFGVYTKVSAYLNWYNNWKAEK 432
```

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RESULT 14
US-10-184-642-330
/ Sequence 330, Application US/10184642
/ Publication No. US20030157635A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C194
/ CURRENT FILING DATE: 2002-06-27
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 330
/ LENGTH: 432
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-184-642-330

Query Match          79.1%; Score 1266; DB 12; Length 432;
Best Local Similarity 97.4%; Pred. No. 6.3e-117;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 51 KIVGGYALVDSPWQVSIQYDKQHVCGSILDPHWLTAHCFRKHTDVFNNKVRAGSD 110
Db 199 RVVGGEEASVDSWPQVSIQYDKQHVCGSILDPHWLTAHCFRKHTDVFNNKVRAGSD 258

QY 111 KLGSPFLAVAKIIIEFNPMYPKNDIALMKLOFPLTFSGTVPICLPFFDEELTPATP 170
```

```
Db 259 KLGSPFLAVAKIIIEFNPMYPKNDIALMKLOFPLTFSGTVPICLPFFDEELTPATP 318

QY 171 LWTIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAVQGEVTEKMKCAGIPEGGVDTTC 230
Db 319 LWTIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAVQGEVTEKMKCAGIPEGGVDTTC 378

QY 231 QGDSGGPLMYQSDQHWVGVISWGYCGGSPSTFGVYTKVSAYLNWYNNWKAEK 284
Db 379 QGDSGGPLMYQSDQHWVGVISWGYCGGSPSTFGVYTKVSAYLNWYNNWKAEK 432

RESULT 15
US-10-196-747-330
/ Sequence 330, Application US/10196747
/ Publication No. US20030162250A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C346
/ CURRENT FILING DATE: 2002-07-16
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 330
/ LENGTH: 432
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-196-747-330

Query Match          79.1%; Score 1266; DB 12; Length 432;
Best Local Similarity 97.4%; Pred. No. 6.3e-117;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 51 KIVGGYALVDSPWQVSIQYDKQHVCGSILDPHWLTAHCFRKHTDVFNNKVRAGSD 110
Db 199 RVVGGEEASVDSWPQVSIQYDKQHVCGSILDPHWLTAHCFRKHTDVFNNKVRAGSD 258

QY 111 KLGSPFLAVAKIIIEFNPMYPKNDIALMKLOFPLTFSGTVPICLPFFDEELTPATP 170
Db 259 KLGSPFLAVAKIIIEFNPMYPKNDIALMKLOFPLTFSGTVPICLPFFDEELTPATP 318

QY 171 LWTIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAVQGEVTEKMKCAGIPEGGVDTTC 230
Db 319 LWTIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAVQGEVTEKMKCAGIPEGGVDTTC 378

QY 231 QGDSGGPLMYQSDQHWVGVISWGYCGGSPSTFGVYTKVSAYLNWYNNWKAEK 284
Db 379 QGDSGGPLMYQSDQHWVGVISWGYCGGSPSTFGVYTKVSAYLNWYNNWKAEK 432
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Search completed: December 2, 2003, 02:51:18
Job time : 218.096 secs

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ein search, using sw model

(without alignments)
580.377 Million cell updates/sec

Title: US-09-607-745-9

Perfect score: 1600

Sequence: 1 MDSKGSSQKSRLLLLVSN.....LNWIYNVWKAELSRHHHHH 292

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq Length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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1: /cqn2 6/ptodata/2/iaa/5A COMB.pcp:*

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2: /cgn2 6/ptodata/2/iaa/5B COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1266	79.1	423	3	US-09-656-002-2		Sequence 2, Appli
2	1266	79.1	435	4	US-09-008-2718-6		Sequence 6, Appli
3	765	47.8	316	4	US-09-387-375-9		Sequence 9, Appli
4	754.5	47.2	315	4	US-09-386-653A-9		Sequence 9, Appli
5	746	46.6	328	4	US-09-386-642-11		Sequence 11, Appli
6	740.5	46.3	327	4	US-09-386-629-8		Sequence 8, Appli
7	672.5	42.0	289	4	US-09-386-642-14		Sequence 14, Appli
8	645	40.3	288	4	US-09-386-642-13		Sequence 13, Appli
9	601.5	37.6	306	4	US-09-386-642-53		Sequence 53, Appli
10	593	37.1	319	4	US-09-386-642-12		Sequence 12, Appli
11	574	35.9	284	4	US-09-386-642-54		Sequence 54, Appli
12	526.5	32.9	418	1	US-08-508-4480-25		Sequence 25, Appli
13	526.5	32.9	418	4	US-09-370-838-82		Sequence 82, Appli
14	526.5	32.9	418	4	US-09-370-838-83		Sequence 83, Appli
15	524.5	32.8	418	4	US-09-370-838-62		Sequence 62, Appli
16	522.5	32.7	232	1	US-08-508-4480-19		Sequence 19, Appli
17	507	31.7	454	3	US-09-518-046-2		Sequence 2, Appli
18	506	31.6	492	3	US-09-342-749-2		Sequence 2, Appli
19	506	31.6	492	4	US-09-691-840-2		Sequence 2, Appli
20	505.5	31.6	376	4	US-09-820-002-2		Sequence 2, Appli
21	505.5	31.6	417	4	US-09-820-002-4		Sequence 4, Appli
22	499.5	31.2	256	2	US-09-027-337-3		Sequence 3, Appli
23	499.5	31.2	256	4	US-09-644-600-3		Sequence 3, Appli
24	497.5	31.1	255	3	US-08-944-483-67		Sequence 67, Appli
25	497	31.1	283	3	US-08-807-151-1		Sequence 1, Appli
26	497	31.1	283	4	US-09-478-957-1		Sequence 1, Appli
27	491.5	30.7	416	2	US-09-000-846-2		Sequence 2, Appli

```
/ Sequence 6, Application US/09008271A
/ Patent No. 6203979
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ Hillman, Jennifer L.
/ Yue, Henry
/ Guegler, Karl J.
/ Corley, Neil C.
/ Tang, Tom Y.
/ Shah, Purvi
/ TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
/ NUMBER OF SEQUENCES: 24
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Dr.
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: fasmseq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/008,271A
/ FILING DATE: 16-Jan-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: <Unknown>
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mohan-Peterson, Sheela
/ REGISTRATION NUMBER: 41,201
/ REFERENCE/DOCKET NUMBER: PF-0458 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 435 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: COLNOT13
/ CLONE: 1337018
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-008-271A-6

Query Match 79.1%; Score 1266; DB 3; Length 435;
Best Local Similarity 97.4%; Pred. No. 5,7e-128;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 51 KIVGGYALDVSQWVSIQYDKQHVCGGSLDHPHVLTAACHCRKHTDYNKVRAGSD 110
Db 202 RVVGEASVDSWQVSIQYDKQHVCGGSLDHPHVLTAACHCRKHTDYNKVRAGSD 261
QY 111 KLGSPFLSAVAKIIIBFNPMYKDNIDIALMKLOPPLTFSGTVRPICLPFFDELTATP 170
Db 262 KLGSPFLSAVAKIIIBFNPMYKDNIDIALMKLOPPLTFSGTVRPICLPFFDELTATP 321
QY 171 LWIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAVQGEVTEKMKVAGIPGGVDT 230
Db 322 LWIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAVQGEVTEKMKVAGIPGGVDT 381
QY 231 QGDSGGLPMQSDQWVGVIVSWGCGGSPSTPGYTKVSAYLNWIYNWKAEL 284
Db 382 QGDSGGLPMQSDQWVGVIVSWGCGGSPSTPGYTKVSAYLNWIYNWKAEL 435

RESULT 3
US-09-387-375-9
/ Sequence 9, Application US/09387375
/ Patent No. 6485957
/ GENERAL INFORMATION:
/ APPLICANT: Darrow, Andrew
/ Applicant: Andrade-Gordon, Patricia
/ APPLICANT: Qi, Jenson
/ TITLE OF INVENTION: DNA Encoding the Human Serine
/ FILE REFERENCE: ORT-1031
/ CURRENT APPLICATION NUMBER: US/09/387,375
/ CURRENT FILING DATE: 1999-08-31
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: Patent in Ver. 2.0
/ SEQ ID NO 9
/ LENGTH: 316
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Amino acid
/ OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-09-387-375-9

Query Match 47.8%; Score 765; DB 4; Length 316;
Best Local Similarity 51.1%; Pred. No. 3.4e-74;
Matches 164; Conservative 38; Mismatches 85; Indels 34; Gaps 10;

QY 1 MDSKSSQKSRLLLLVSVNLLLCQGVSDYKDDDDVDAALAAPDDDDKIVGGYALDV 60
Db 1 MDSKSSQKSRLLLLVSVNLLLCQGVSDYKDDDDVDAALAAPDDDDKIVGGYALDV 60
QY 61 DSWPMQVSIQYDKQHVCGGSLDHPHVLTAACHCRKHTDYNKVRAGSDKLGSPF 116
Db 61 GEWPMQVSIQYDKQHVCGGSLDHPHVLTAACHCRKHTDYNKVRAGSDKLGSPF 120
QY 117 SLAVAKIIIBFNPMYKDNIDIALMKLOPPLTFSGTVRPICLPFFDELTATP 173
Db 121 SVEPRVLL--PFDYSEGDGARGDLALLQRRPVLSARQVPVCLPVGARPPGTPCRV 177
QY 174 IGMGFTKQNGKMSD--ILLQASVQVIDSTRCN--ADDAYQGE--VTEKMKVAGI 224
Db 178 TGMG-SLRFGVPLPEWRPLQGVVPLDSDTCDGLVHVGADVPQAEIVLPGSLCAGY 236
QY 225 GGVDTCQGSQGLP-MYQSDQWVGVIVSWGCGGSPSTPGYTKVSAYLNWI----- 276
Db 237 GHKDACQGSQGLPCLQSGSWLVGVSWGKSCALPNRPVTVTSVATISPMQARVTSN 296
QY 277 -----YNNWKAELSRHHHHH 292
Db 297 ASRYPYDV-PDYAARHHHHH 316

RESULT 4
US-09-386-653A-9
/ Sequence 9, Application US/09386653A
/ Patent No. 6458564
/ GENERAL INFORMATION:
/ APPLICANT: Darrow, Andrew
/ Applicant: Andrade-Gordon, Patricia
/ APPLICANT: Qi, Jian-shen
/ TITLE OF INVENTION: DNA encoding the novel human serine
/ FILE REFERENCE: ORT-1032
/ CURRENT APPLICATION NUMBER: US/09/386,653A
/ CURRENT FILING DATE: 1999-08-31
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: Patent in Ver. 2.0
/ SEQ ID NO 9
/ LENGTH: 315
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
/ OTHER INFORMATION: of Protease T in a zymogen activation construct
US-09-386-653A-9
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Query Match 47.2%; Score 754.5; DB 4; Length 315;
Best Local Similarity 48.4%; Pred. No. 4.6e-73;
Matches 156; Conservative 46; Mismatches 83; Indels 37; Gaps 10;

QY 1 MDSKSSQSRLLLLLVSNLLLCQGVSDYKDDDDVDAALAAPDDDDKIVGGYALDV 60
DB 1 MDSKSSQSRLLLLLVSNLLLCQGVSDYKDDDDVDAALAAPDDDDKIVGGYALDV 60

QY 61 DSWPMQVSIQYDKQHVCGGSIIDPHWVLTAAHCFRKHDTDFNWKVRAGSDKL-GSFPFSLA 119
DB 61 GSWPMQVSIQYDKQHVCGGSIIDPHWVLTAAHCFRKHDTDFNWKVRAGSDKL-GSFPFSLA 120

QY 120 VAKIIIEFNPMYK---PKNDALMKIQPLPFGVTRPCLPFPFDEELTPATEL--WII 174
DB 121 YARVROVENPLQYGTASSADVALVEAPVPTNYILPVCLP--DPSVIFETGMCMWT 178

QY 175 GWGFTKQNGKMSD-----ILQASVQVIDSTRCN-----ADDAYQGE-VTERKMCAG 221
DB 179 GWSGSPSE-----EDLLPEPRILQKLAVPIDTPKCNLLYSKDTFPGYQPKTIKNDMLCAG 233

QY 222 IPEGGVDTCCGDSGGPLMYQSDQ-WHVGVISWGYCGGSPSTPGVYTKVSAYLNWYV- 279
DB 234 FREGKXDAKSGGSLVCLVGSQSLQAGVISWEGCARGQRNPGVYIRVTAHHNWIHRII 293

QY 280 -----WKAELSRHHHHH 292
DB 294 PKLQFQPARLGQKSRHHHHH 315

RESULT 5
US-09-386-642-11
; Sequence 11, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-11

Query Match 46.8%; Score 746; DB 4; Length 328;
Best Local Similarity 49.7%; Pred. No. 4e-72;
Matches 163; Conservative 35; Mismatches 94; Indels 36; Gaps 8;

QY 1 MDSKSSQSRLLLLLVSNLLLCQGVSDYKDDDDVDAALAAPDDDDKIVGGYALDV 60
DB 1 MDSKSSQSRLLLLLVSNLLLCQGVSDYKDDDDVDAALAAPDDDDKIVGGYALDV 60

QY 61 DSWPMQVSIQYDKQHVCGGSIIDPHWVLTAAHCFRKHDTDFNWKVRAGSDKL-GSFPFSLA- 119
DB 61 GQPMQVSIYGVHVHVGCGSLVSEQWLSAAHCFPSEHHEAVEVKGARHQLDSYSEDAK 120

QY 120 VAKIIIEFNPMYK---NDIALMKIQPLPFGVTRPCLPFPFDEELTPATELMIIGW 176
DB 121 VSTLKDIIPHSYLOQSSQDIALQLSRPITSRYIRPCLPAANASFPNGLHCITVGW 180

QY 177 GFTKQNGKMS-DILQASVQVIDSTRCN-----DDAYQGE---VTERKMCAGIPEGGVD 229
DB 181 GHVAPSVSLTPKLOQLEVLISRETNCNLYNIDAKPEPFPVQEDVMVCAGYVEGGKA 240
```

```
QY 230 CQDSSGGPLMYQSD-QWHVGVISWGYCGGSPSTPGVYTKVSAYLNWY----- 277
DB 241 CQDSSGGPLSCPEVGLWLTGIVSWGDACGARNRGVTVTLASSYASWQSKVTELOPRVV 300

QY 278 -----NWKAEEL---SRHHHHH 292
DB 301 PQTQSSQSDSNLCGSHLAPSSRRHHHHH 328

RESULT 6
US-09-386-629-8
; Sequence 8, Application US/09386629
; Patent No. 6426139
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L.
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Identification and Characterization of the complementary
; FILE REFERENCE: ORT-1030
; CURRENT APPLICATION NUMBER: US/09/386,629
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C-E catalytic
; OTHER INFORMATION: domain fusion protien
US-09-386-629-8

Query Match 46.3%; Score 740.5; DB 4; Length 327;
Best Local Similarity 49.8%; Pred. No. 1.6e-71;
Matches 164; Conservative 39; Mismatches 87; Indels 39; Gaps 10;

QY 1 MDSKSSQSRLLLLLVSNLLLCQGVSDYKDDDDVDAALAAPDDDDKIVGGYALDV 60
DB 1 MDSKSSQSRLLLLLVSNLLLCQGVSDYKDDDDVDAALAAPDDDDKIVGGYALDV 60

QY 61 DSWPMQVSIQYDKQHVCGGSIIDPHWVLTAAHCFRKHDTDFNWKVRAGSDKL-GSFPFSLA 119
DB 61 SEWPMVSIQKNGTHCAGSLTSRWVITAAHCFKDNLMKPYLSVLLGAWQLGN-PGSR 119

QY 120 VAKIII--IEFNPMYK---DIALMKIQPLPFGVTRPCLPFPFDEELTPATELMI 173
DB 120 SOKVGVAWVEPHVPSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWI 179

QY 174 ICGWFTKQNGKMS--SDILQASVQVIDSTRCN-----DDAYQGEVTERKMCAGIPEGGVD 228
DB 180 SWG-SIQGVLPHPQTLQKVLIIIDSEVCHYWRGAGGQGITDMLCAGYLEGERD 238

QY 229 CQDSSGGPLMYQSD-QWHVGVISWGYCGGSPSTPGVYTKVSAYLNWYVWK----- 281
DB 239 ACLGDSGGPLMCQVDGAMLLAGIISWEGCAERNRPGVVISLSAHSWSWEKIVQGVQLRG 298

QY 282 -----AELSRHHHHH 292
DB 299 RAQGGGALRAPSGSGAAARSRRHHHHH 327

RESULT 7
US-09-386-642-14
; Sequence 14, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
```



```

; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-12

Query Match 37.1%; Score 593; DB 4; Length 319;
Best Local Similarity 44.2%; Pred. No. 1.2e-55;
Matches 133; Conservative 35; Mismatches 95; Indels 38; Gaps 9;

QY 28 VSDYKDDDDVDAALAAPDDDDKIVGGYALDVDSWFPQWVSIQYDKQHVCGGSLDPHWV 87
DB 21 VPDYKDDDD--DAAALAAPDDDDKIVGGYALEAGQWQVSIYEGVHVCGGSLVSEQWV 78

QY 88 LPAAHCFRKHDTVFNKVRAGSKLGSFPPLA-VAKIIIEFNPMPYKQD---NDIALMKL 143
DB 79 LSAHCFPSEHHEKAEVEKLGARHQLDSYSEDAKVSTIKDIIPSPYLVQSGQGDIALQL 138

QY 144 QPLTSGTVRPICLPFPFDEELTPATPLWIGFTKQNGKMS-DILLQASVQVIDSTR 202
DB 139 SRPIITSRYRPICLPAANASFPNGLHCTVTGWHVAPSVSLTLPKQLQLEVLISRET 198

QY 203 CNA---DDAYQGE---VTEKMMGAGIPGEGVDTCQDSDGSGPLMQSD-QHVVGVISWGY 255
DB 199 CNCLYNIDAKPEEPHFHFOEDMVCAGYEGGKACQDSDGGPLSCPVEGLMYLTGIVSWG 258

QY 256 GCGGPGTGGVYTKVSAVLNWIY-----NVKAEI---SRHHHHH 291
DB 259 ACGARNRPGVYTLASSVSIQSKVTELPQVVPQTQESQPDNSLCSHLAFSSRRHHHH 318

QY 292 H 292
DB 319 H 319

RESULT 11
US-09-386-642-54
; Sequence 54, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human ME2
; OTHER INFORMATION: protease in PREK zymogen vector
US-09-386-642-54

Query Match 35.9%; Score 574; DB 4; Length 284;
Best Local Similarity 44.2%; Pred. No. 1.1e-53;
Matches 133; Conservative 39; Mismatches 103; Indels 26; Gaps 11;

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QY 1 MDSKSSOKSRLLLLLVSNLLLCQGVSDYKDDDDVDAALAAPDDDDKIVGGY-ALD 59
DB 1 MDSKSSOKSRLLLLLVSNLLLCQGVSDYKDDDDVDAALAAPDDDDKIVGGYNCLE 60

QY 60 VDSWFPQWVSIQYDKQHVCGGSLDPHWVLTAAHCFRKHDTVFNKVRAGSDKL--GSFPS 117
DB 61 PHSQWPQAALVMENELFCSGVLVHPQWVLSAHCFTQN-----SYTIGLGLHSLEADQEPG 115

QY 118 LAVAKIIIEFNPMPYKQD---NDIALMKLQPLTSGTVRPICLPFPFDEELTPATPLWII 174
DB 116 SQMVEASLSVRHPEYNRPPLANDLMLIKLDESVSBSDTIRISIA--SOCPAGNSCLVS 173

QY 175 WGFTKQNGKMSDILLQASVOVIDSTRCNA--DDAYQGEVTEKMMGAGIPGEGVDTCQ 232
DB 174 GWGLLA--NGRMPYTLQCVNVSVSEEVCSKLYDPLIY-----PSMFCAGGHDQKDCSCNG 227

QY 233 DSGGPIMQSDQWVHVGVISWGYG-CGGPSTPGVYTKVSAVLNWIYNVKAELSRHHHHH 291
DB 228 DSGGPLICNG---YLQGLVSPFGKAPCGQGVGVYTNLCKFTIEWIEKTVQAS-SRHHHHH 283

QY 292 H 292
DB 284 H 284

RESULT 12
US-08-508-448C-25
; Sequence 25, Application US/08508448C
; Patent No. 5804410
; GENERAL INFORMATION:
; APPLICANT: Kazuyoshi YAMAOKA et al.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING
; TITLE OF INVENTION: TRYPsin-LIKE ENZYME AND PROCESS FOR PRODUCING THE ENZYME
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,448C
; FILING DATE: July 28, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 418 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-508-448C-25

Query Match 32.9%; Score 526.5; DB 1; Length 418;
Best Local Similarity 41.8%; Pred. No. 2.5e-48;
Matches 97; Conservative 49; Mismatches 79; Indels 7; Gaps 4;

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Db 302 PGSTAYVTGWAQYAGHTYPE-LRQGGVRIISNDVNCNAPHSYNGAILSGMLCAGVPOGG 360

Qy 227 VDTCCGDSGGPLMYOSDQ--WHVVGIVSWGYCGGSPSTPGVYTKVSAKLNWI 276

Db 361 VDACQCGDSGGPLVQEDSRRLWFIVGIVSWGDQGLFDKFGVYTRVTAXIDWI 412

Search completed: December 2, 2003, 02:31:10
Job time : 22.2875 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 2, 2003, 02:42:05 : Search time 262.68 Seconds

(without alignments)

3662.446 Million cell updates/sec

Title: US-09-607-745-9

Perfect score: 1600

Sequence: 1 MDSKSSQSRLLLLVVS.....LNWIYNVWKAELSRHHHHH 292

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 2190069 segs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPRO.spool_p/US09607745/runat_01122003_160940_10006/app.query.fasta_1.1038
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZB=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09607745@cgn_1_123@runat_01122003_160940_10006
-NCPU=6 -ICPU=3 -NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=130 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1266	79.1	2038	12 US-10-180-719-18

2	1266	79.1	2063	11 US-09-888-257A-2	Sequence 2, Appli
3	1266	79.1	2063	11 US-09-948-374-274	Sequence 274, App
4	1266	79.1	2063	12 US-10-015-387A-274	Sequence 274, App
5	1266	79.1	2063	12 US-10-063-735-111	Sequence 111, App
6	1266	79.1	2063	12 US-10-006-130A-274	Sequence 274, App
7	1266	79.1	2063	12 US-10-199-672-329	Sequence 329, App
8	1266	79.1	2063	12 US-10-006-172A-274	Sequence 274, App
9	1266	79.1	2063	12 US-10-187-749-329	Sequence 329, App
10	1266	79.1	2063	12 US-10-194-457-329	Sequence 329, App
11	1266	79.1	2063	12 US-10-184-642-329	Sequence 329, App
12	1266	79.1	2063	12 US-10-196-747-329	Sequence 329, App
13	1266	79.1	2063	12 US-10-015-392A-274	Sequence 274, App
14	1266	79.1	2063	12 US-10-017-253A-274	Sequence 274, App
15	1266	79.1	2063	12 US-10-173-689-329	Sequence 329, App
16	1266	79.1	2063	12 US-10-173-690-329	Sequence 329, App
17	1266	79.1	2063	12 US-10-173-691-329	Sequence 329, App
18	1266	79.1	2063	12 US-10-173-692-329	Sequence 329, App
19	1266	79.1	2063	12 US-10-173-693-329	Sequence 329, App
20	1266	79.1	2063	12 US-10-173-694-329	Sequence 329, App
21	1266	79.1	2063	12 US-10-173-695-329	Sequence 329, App
22	1266	79.1	2063	12 US-10-173-696-329	Sequence 329, App
23	1266	79.1	2063	12 US-10-173-697-329	Sequence 329, App
24	1266	79.1	2063	12 US-10-174-569-329	Sequence 329, App
25	1266	79.1	2063	12 US-10-174-583-329	Sequence 329, App
26	1266	79.1	2063	12 US-10-174-589-329	Sequence 329, App
27	1266	79.1	2063	12 US-10-174-591-329	Sequence 329, App
28	1266	79.1	2063	12 US-10-175-736-329	Sequence 329, App
29	1266	79.1	2063	12 US-10-175-742-329	Sequence 329, App
30	1266	79.1	2063	12 US-10-175-744-329	Sequence 329, App
31	1266	79.1	2063	12 US-10-175-745-329	Sequence 329, App
32	1266	79.1	2063	12 US-10-175-748-329	Sequence 329, App
33	1266	79.1	2063	12 US-10-175-751-329	Sequence 329, App
34	1266	79.1	2063	12 US-10-175-754-329	Sequence 329, App
35	1266	79.1	2063	12 US-10-176-480-329	Sequence 329, App
36	1266	79.1	2063	12 US-10-176-489-329	Sequence 329, App
37	1266	79.1	2063	12 US-10-176-754-329	Sequence 329, App
38	1266	79.1	2063	12 US-10-176-755-329	Sequence 329, App
39	1266	79.1	2063	12 US-10-176-759-329	Sequence 329, App
40	1266	79.1	2063	12 US-10-176-920-329	Sequence 329, App
41	1266	79.1	2063	12 US-10-176-923-329	Sequence 329, App
42	1266	79.1	2063	12 US-10-176-924-329	Sequence 329, App
43	1266	79.1	2063	12 US-10-176-984-329	Sequence 329, App
44	1266	79.1	2063	12 US-10-179-508-329	Sequence 329, App
45	1266	79.1	2063	12 US-10-179-512-329	Sequence 329, App

ALIGNMENTS

RESULT 1

US-10-180-719-18
; Sequence 18, Application US/10180719
; Publication No. US20030166246A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
FILING NUMBER: US/10/180,719
FILING DATE: 25-Jun-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271
FILING DATE: 16-Jan-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLNNOT13
CLONE: 1337018
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-180-719-18

Alignment Scores:

Pred. No.:	1,648-152	Length:	2038
Score:	1266.00	Matches:	228
Percent Similarity:	98.29%	Conservative:	2
Best Local Similarity:	97.44%	Mismatches:	4
Query Match:	79.12%	Indels:	0
DB:	12	Gaps:	0

US-09-607-745-9 (1-292) x US-10-180-719-18 (1-2038)

Qy	51	LysLeuValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln	70
Db	803	CGTGTGGTGGTGGGAGGAGGCGCTCTGTGGATTCTTGGCCCTGGCAGGTGAGCATCCAG	862
Qy	71	TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla	90
Db	863	TACGACAAACAGCAGCTGTGGAGGAGGAGCACTCGGACCCCACTGGGTCTTCACGGCA	922
Qy	91	AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp	110
Db	923	GCCCACTGCTTCAGGAAACATACCGATGTGTTCACTGGAAGGTGGGCGAGGCTCAGAC	982
Qy	111	LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleIleGluPheAsnPro	130
Db	983	AAACTGGGCGAGTTCCTCCCATCCCTGGCTGTGGCCAGATCATCATATTGAATTCACCC	1042
Qy	131	MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer	150
Db	1043	ATGTACCCCAAGACAAATGACATCGCCCTCATGAGCTGCGATCCCACTCACTTTCTCA	1102
Qy	151	GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro	170
Db	1103	GGCAGAGTCAGGCCCATCTGTGCTTCTTGTATGAGGAGCTCACTCCAGCCACCCCA	1162
Qy	171	LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu	190
Db	1163	CTCTGGATCGATGGATGGGCTTTACGAGGAGAGATGGAGGAGATCTGTGACATATG	1222
Qy	191	LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaThrGln	210
Db	1223	CTGACGGGCTGAGTCAGGTGATTCAGACGACACCGTGCATGTCAGACATGCGTACCG	1282
Qy	211	GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys	230
Db	1283	GGGGAAGTCACCGAAGATGATGTGTCAGGCATCCCGGAAGGGGTGTGACACCTGC	1342
Qy	231	GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle	250

Db	1343	CAGGTGACAGTGTGGGCCCTGATGTACCAATCTGACCATGTGGTGGCATC	1402
Qy	251	ValSerTrpGlyTyrGlyCysGlyProSerThrProGlyValTyrThrLysValSer	270
Db	1403	GTTAGCTGGGGCTATGGCTGCGGGGCCGAGCACCCGAGGATATACACCAAGGTCTCA	1462
Qy	271	AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu	284
Db	1463	GCCTATCTCACTGATCTACATGTCTGGAGGCTGAGCTG	1504

RESULT 2

US-09-888-257A-2
; Sequence 2, Application US/09888257A
; Publication No. US20030060612A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Polakis, Paul
; APPLICANT: Smith, Victoria
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5002R1
; CURRENT APPLICATION NUMBER: US/09/888,257A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/063,540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: US 60/089,653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/099,792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/103,678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: US 60/235,451
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-888-257A-2

Alignment Scores:
Pred. No.: 1,678-152 Length: 2063
Score: 1266.00 Matches: 228
Percent Similarity: 98.29% Conservative: 2
Best Local Similarity: 97.44% Mismatches: 4
Query Match: 79.12% Indels: 0
DB: 11 Gaps: 0

US-09-607-745-9 (1-292) x US-09-888-2574-2 (1-2063)

QY 51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
Db 804 CGTGTGGTGGTGGGAGGAGGCTCTGTGGATTCTTGGCTTGGCAGGTCAGCATCCAG 863
QY 71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
Db 864 TAGACAAACAGACAGCTCTGTGGAGGAGGAGCATCTTGGACCCCACTGGTCTCCAGGCA 923
QY 91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
Db 924 GCCCACTGCTTCAGGAAACATACGATGTGTTCACCTGGAAGGTGGCGGAGGCTCAGAC 983
QY 111 LysLeuGlySerPheProSerLeuAlaValAlaLysIlellellellelleGluPheAsnPro 130
Db 984 AAACCTGGGAGCTTCCCATCCCTGGCTGTGGCCAAAGATCATCATTAATTCACCC 1043
QY 131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
Db 1044 ATGTACCCCAAGACATGATCATCGCCCTCATGAAGCTGCAGTTCCCACTCATTTCTCA 1103
QY 151 GlyThrValArgProIleCysLeuProPhePheAspGluLeuThrProAlaThrPro 170
Db 1104 GGCACAGTCAGGCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1163
QY 171 LeuTrpIlellelleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu 190
Db 1164 CTCGTGATCATTTGATGGGCTTTACGAAGCAGATGGAGGAAGATGTCTGACATATCTG 1223
QY 191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210
Db 1224 CTGACGGCTGATCCAGCTCATTTGACAGCACAGTGTGCATGACAGAGTGGTACAG 1283
QY 211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 230
Db 1284 GGGGAAGTCACCGAGAAGATGATGTGTGACGATCCCGGAAGGGGTGGACACCTGC 1343
QY 231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 250
Db 1344 CAGGGTGACAGTGTGGGCCCTCATGTATCAATCTGACCAAGTGGCATGTGGTGGCATC 1403
QY 251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
Db 1404 GTTAGCTGGGGCTATGCTGCGGGGCCCGAGACCCCGAGAGTATACACCAAGTCTCA 1463
QY 271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
Db 1464 GCCTATCTCAACTGGATCTACATGTCTGGAAGGCTGAGCTG 1505

RESULT 3

US-09-946-374-274

; Sequence 274, Application US/09946374

; Publication No. US20030073129A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
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; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
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; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-15
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; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848

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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
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; PRIOR APPLICATION NUMBER: 60/101014
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; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
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; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores:
Pred. No.: 1.67e-152 Length: 2063
Score: 1266.00 Matches: 228
Percent Similarity: 98.29% Conservative: 2
Best Local Similarity: 97.44% Mismatches: 4
Query Match: 79.12% Indels: 0
DB: 11 Gaps: 0

US-09-607-745-9 (1-292) x US-09-946-374-274 (1-2063)
QY 51 LysileValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
DB 804 CGTGTGGTGGTGGGAGGAGGCTCTGTGGATTCTTGGCTTGGCTTGGAGGTGAGTATCCAG 863
QY 71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
DB 864 TACGACAAACAGCACGCTGTGTGGAGGAGCATCTCTGGACCCGCCACTGGGTCTCCACGGCA 923
QY 91 AlahisCysPheArxLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
DB 924 GCCACGTCTTCAGAAACATACCGATGTGTCACTGGAAGGTGGCGGAGGTTCAGAC 983
QY 111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 130
DB 984 AAACCTGGCAGCTTCCCATCTCTGGCTGTGGCCAGATCATCATCATCATGATTCAACCCC 1043
QY 131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
DB 1044 ATGTACCCCAAGACAATGACATCGCCCTCATGAAGTGCAGTTCACACTCCTTCTCTCA 1103
QY 151 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 170
DB 1104 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTCATGAGGAGCTCACTCCAGCCACCCCA 1163
QY 171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 190
DB 1164 CTCGTGATCATTTGGATGGGGCTTTACGAGCAGATGGAGGAGAGATGCTCTGACATCTG 1223
QY 191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrGln 210
```

Db 1224 CTGAGCGCTCAGTCCAGTTCATTCAGACACACGCGTGCATCCAGACGATCGGTACCAG 1283
QY 211 GlyGluValThrGluLysMetMetCysAlaGlyLeuProGluGlyGlyValAspThrCys 230
Db 1284 GGGGAAGTCCACGAGAGATGATGTGTGAGGATCCCGAAGGGGGTGTGGACACCTGC 1343
QY 231 GluGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTyrHisValValGlyLeu 250
Db 1344 CAGGTGACAGTGTGGGCCCCCTGATGATACCAATCTCAGCAGTGGCAATGTGGTGGGCATC 1403
QY 251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
Db 1404 GTTAGCTGGGGCTATGCTGGGGGGGGCGGAGCACCCAGAGATATACACCRAGTCTCA 1463
QY 271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
Db 1464 GCCTATCTCACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505

RESULT 4

US-10-015-387A-274
; Sequence 274, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 274
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-387A-274

Alignment Scores:
Pred. No.: 1.67e-152 Length: 2063
Score: 1266.00 Matches: 228
Percent Similarity: 98.29% Conservative: 2
Best Local Similarity: 97.44% Mismatches: 4
Query Match: 79.12% Indels: 0
DB: 12 Gaps: 0

US-09-607-745-9 (1-292) x US-10-015-387A-274 (1-2063)

QY 51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTyrGlnValSerIleGln 70
Db 804 CGTGTGGTGGTGGGAGAGCGCTCTGTGGATCTTGGCCTTGGCAGTCCAGATCCAG 863
QY 71 TyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAla 90
Db 864 TACGACAAACAGCAGCTCTGTGGAGGAGCATCTGGACCCCCACTGGTCTCTCAGCGCA 923
QY 91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
Db 924 GCCCACTGCTTCAGGAACATACCGATGTGTTCACATGGAAGTGGCGGCGAGGCTCAGAC 983

QY 111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 130
Db 984 AAACCTGGGAGCTTCCATCCCTGGCTGTGGCCAGATCATCATTTGAATTCACACCC 1043
QY 131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
Db 1044 ATGTACCCCAAGACAAATGACATCGCCCTCATGAAGCTGCAGTTCACACTCTTCTCA 1103
QY 151 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProIleThrPro 170
Db 1104 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGAGGCTCATCTCCAGCCACCCCA 1163
QY 171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 190
Db 1164 CTCTGATCATTTGGATGGGCTTTTACAGACGAATGGAGGAGAGATGCTGTGACTACTG 1223
QY 191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210
Db 1224 CTCAGGGGCTCAGTCCAGGTCATTGACAGCACACGCGTGCANTGCAGACGATGGTACCAG 1283
QY 211 GlyGluValThrGluLysMetMetCysAlaGlyLeuProGluGlyGlyValAspThrCys 230
Db 1284 GGGGAAGTCCACGAGAGATGATGTGTGACAGGATCCCGAAGGGGTGTGGACACCTGC 1343
QY 231 GluGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyLeu 250
Db 1344 CAGGTGACAGTGTGGCCCCCTGATGATCAATCTGACCGTGGCATGTGGTGGGCATC 1403
QY 251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
Db 1404 GTTAGCTGGGGCTATGCTGGGGGGGGCGGAGCACCCAGAGATATACACCRAGTCTCA 1463
QY 271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
Db 1464 GCCTATCTCACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505

RESULT 5

US-10-063-735-111
; Sequence 111, Application US/10063735
; Publication No. US20030138882A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: F3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,735
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 111
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-063-735-111

Alignment Scores:
Pred. No.: 1.67e-152 Length: 2063
Score: 1266.00 Matches: 228
Percent Similarity: 98.29% Conservative: 2
Best Local Similarity: 97.44% Mismatches: 4
Query Match: 79.12% Indels: 0
DB: 12 Gaps: 0

US-09-607-745-9 (1-292) x US-10-063-735-111 (1-2063)

```
Qy 51 LysLeuValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
    : : : : :
Db 804 CGTGTGGTGGTGGGAGGAGCCCTCTGTGGATTCTTGGCCCTTGGCAGGTGAGCATCCAG 863

Qy 71 TyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAla 90
    : : : : :
Db 864 TACGACAAACAGCAGCTGTGTGGAGGAGCATCTGTGGAGGAGCATCTGTGACCCCTGGTCTCAGGCCA 923

Qy 91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
    : : : : :
Db 924 GCCACTGCTTCAGAAACATACCGATGTGTTCACCTGGAAGGTGCGGGCAGGCTCAGAC 983

Qy 111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 130
    : : : : :
Db 1164 CTCTGGATCATTGGATGGGCTTTACGAAGCAGAGATGCGAGGAGCATCTCATTTCTCA 1223

Qy 121 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 170
    : : : : :
Db 1104 GGCACAGTCAGCCCATCTGTCTGCCCTTCTTGTATGAGAGCTCACTCCAGCCACCCCA 1163

Qy 171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu 190
    : : : : :
Db 1164 CTCTGGATCATTGGATGGGCTTTACGAAGCAGAGATGCGAGGAGCATCTCATTTCTCA 1223

Qy 191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrGln 210
    : : : : :
Db 1224 CTGAGGCGTCAGTCCAGTCAATTGACAGCACCGGTGCAATGCGAGAGCATGCGTACCAG 1283

Qy 211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyValAspThrCys 230
    : : : : :
Db 1284 GGGAGCTCACCGAAGATGATGTGTGAGCATCCCGGAGGGGTGTGACACCTGCG 1343

Qy 231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 250
    : : : : :
Db 1344 CAGGCTGACAGTGTGGGCGCCCTGATGTACCAATCTGACCAATGCGAGTGGCATGTGGTGGCATC 1403

Qy 251 ValSerTrpGlyTyrCysGlyProSerThrProGlyValTyrThrLysValSer 270
    : : : : :
Db 1404 GTTAGCTGGGCTATGGCTGCGGGGCGCGAGCACCCCGAGGAGTATACACCAAGTCTCA 1463

Qy 271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
    : : : : :
Db 1464 GCCTATCTCACTGGATCTACATGTCTGTGAAGGCTGAGCTG 1505
```

RESULT 6

```
US-10-006-130A-274
; Sequence 274, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
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; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 274
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-130A-274

Alignment Scores:
Pred. No.: 1,67e-152 Length: 2063
Score: 1266.00 Matches: 228
Percent Similarity: 98.29% Conservative: 2
Best Local Similarity: 97.44% Mismatches: 4
Query Match: 79.12% Indels: 0
DB: 12 Gaps: 0
```

US-09-607-745-9 (1-232) x US-10-006-130A-274 (1-2063)

```
Qy 51 LysLeuValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
    : : : : :
Db 804 CGTGTGGTGGTGGGAGGAGCCCTCTGTGGATTCTTGGCCCTTGGCAGGTGAGCATCCAG 863

Qy 71 TyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAla 90
    : : : : :
Db 864 TACGACAAACAGCAGCTGTGTGGAGGAGCATCTGTGACCCCTGGTCTCAGGCCA 923

Qy 91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
    : : : : :
Db 924 GCCACTGCTTCAGAAACATACCGATGTGTTCACCTGGAAGGTGCGGGCAGGCTCAGAC 983

Qy 111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 130
    : : : : :
Db 984 AAACCTGGCAGCTTCCCATCCCTGGCTGTGGCCAAAGATCATCATCATTTGAATTCACCCC 1043

Qy 131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
    : : : : :
Db 1044 ATGTACCCCAAGACATGATCATCGCCCTCATGAGCTGCGAGTCCCACTCATCTTCTCA 1103

Qy 151 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 170
    : : : : :
Db 1104 GGCACAGTCAGGCGCATCTGTCTGCCCTTCTTGTATGAGGAGCTCACTCCAGCCACCCCA 1163

Qy 171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu 190
    : : : : :
Db 1164 CTCTGGATCATTGGATGGGCTTTACGAAGCAGAGATGCGAGGAGCATCTCATTTCTCA 1223

Qy 191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrGln 210
    : : : : :
Db 1224 CTGAGGCGTCAGTCCAGTCAATTGACAGCACCGGTGCAATGCGAGAGCATGCGTACCAG 1283

Qy 211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyValAspThrCys 230
    : : : : :
Db 1284 GGGAGGTCACCGAAGATGATGTGTGAGCATCCCGGAGGGGTGTGACACCTGCG 1343

Qy 231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 250
    : : : : :
Db 1344 CAGGCTGACAGTGTGGGCGCCCTGATGTACCAATCTGACCAATGCGAGTGGCATGTGGTGGCATC 1403

Qy 251 ValSerTrpGlyTyrCysGlyProSerThrProGlyValTyrThrLysValSer 270
    : : : : :
Db 1404 GTTAGCTGGGCTATGGCTGCGGGGCGCGAGCACCCCGAGGAGTATACACCAAGTCTCA 1463

Qy 271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
    : : : : :
Db 1464 GCCTATCTCACTGGATCTACATGTCTGTGAAGGCTGAGCTG 1505
```

RESULT 7

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US-10-199-672-329
; Sequence 329, Application US/10199672
; Publication No. US2003014842A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
```

```
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/199,672
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 329
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-199-672-329

Alignment Scores:
Pred. No.: 1.67e-152 Length: 2063
Score: 1266.00 Matches: 228
Percent Similarity: 98.2% Conservative: 2
Best Local Similarity: 97.44% Mismatches: 4
Query Match: 79.12% Indels: 0
DB: 12 Gaps: 0

US-09-607-745-9 (1-292) x US-10-199-672-329 (1-2063)

Qy 51 LysleValGlyGlyTyrAlaLeuAspValAspSerTrpTrpGlnValSerleGln 70
Db 804 CGTGTGGGGTGGGAGAGGCGCTCTGTGGATTCTTGGCTTGGCAGTCCAGTCACG 863
Qy 71 TyrAspLysGlnHisValCysGlyGlySerleLeuAspProHisTrpValLeuThrAla 90
Db 864 TACGACAAACAGCAGCTGTGGAGGAGCATCTGGACCCCTGGCTGGCTCAGGCA 923
Qy 91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
Db 924 GCCCACTGCTTCAGAAACATACCGATGTGTCACTGGAAGTGGCGGAGGCTCAGAC 983
Qy 111 LysLeuGlySerPheProSerLeuAlaValAlaLyslellellelleGluPheAsnPro 130
Db 984 AAACCTGGCAGCTTCCCATCCCTGGCTGGCCCAAGATCATCATTAATCAACCCC 1043
Qy 131 MetTyrProLysAspAsnAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
Db 1044 ATGTACCCCAAGCAATGATGATGCTCATGAGCTGAGTTCACCTCACTTTCTCA 1103
Qy 151 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 170
```

```
Db 1104 GGCACAGTCAAGGCCCATCTCTCTGCCCTTTCTTGTATGAGGAGCTCACTCCAGCCACCCCA 1163
Qy 171 LeuTrpIleleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 190
Db 1164 CTCTGGATCATTTGGATGGGCTTTACGAAGCAGAATGGAGGAAGATGTCTGACATCTG 1223
Qy 191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210
Db 1224 CTGAGGCGCTCAGTCCAGGTCATTCAGCACACGCGTCAATGCAGACGATGCGTACAG 1283
Qy 211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 230
Db 1284 GGGAGGTCAACCGAGAAGATGATGTGTGAGGCAATCCCGAGGGGTGTGGACCTGC 1343
Qy 231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 250
Db 1344 CAGGCTGACAGTGTGGGCGCTCATGTACCAATCTCCAGTGGCATGTGGTGGCATC 1403
Qy 251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTrpThrLysValSer 270
Db 1404 GTTAGCTGGGGCTATGGCTCGGGGGCCCGAGCACCCGAGGATATACACCAAGTCTCA 1463
Qy 271 AlaTyrLeuAsnTrpIleTyrAsnValTrpIleValAlaGluLeu 284
Db 1464 GCCTATCTCACTGGATCTACAAATGTCTGGAAGGCTGAGCTG 1505

RESULT 8
US-10-006-172A-274
; Sequence 274, Application US/10006172A
; Publication No. US20030153000A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C11
; CURRENT APPLICATION NUMBER: US/10/006,172A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
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; PRIOR FILING DATE: 1998-10-26
 ; PRIOR APPLICATION NUMBER: 60/105807
 ; PRIOR FILING DATE: 1998-10-27
 ; PRIOR APPLICATION NUMBER: 60/105881
 ; PRIOR FILING DATE: 1998-10-27
 ; PRIOR APPLICATION NUMBER: 60/105882
 ; PRIOR FILING DATE: 1998-10-27
 ; PRIOR APPLICATION NUMBER: 60/106023
 ; PRIOR FILING DATE: 1998-10-28

Alignment Scores:

Pred. No.: 1,67e-152 Length: 2063
 Score: 1266.00 Matches: 228
 Percent Similarity: 98.29% Conservative: 2
 Best Local Similarity: 97.44% Mismatches: 4
 Query Match: 79.12% Indels: 0
 DB: 12 Gaps: 0

US-09-607-745-9 (1-292) x US-10-006-172A-274 (1-2063)

Qy 51 LysileValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
 Db 804 CGTGTGTGGTGGGGAGGAGGCTCTGTGGATTCTTGGCTTGGCAGGTGAGTCAGATCCAG 863
 Qy 71 TyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAla 90
 Db 864 TAGACAAACAGACAGCTCTGTGGAGGAGGATCTTGACCCCTTGGTCTGGTCTCAGCGCA 923
 Qy 91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
 Db 924 GCCCACTGCTTCAGAAACATACCGATGTGTCACTGGAAGTGGCGGAGGCTCAGAC 983
 Qy 111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 130
 Db 984 AAATGGGACGCTCCATCCCTGGCTGTGGCAGAGATCATCATGATGATCAATCAACCCC 1043
 Qy 131 MetTyrProLysAspAsnAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
 Db 1044 ATGTACCCCAAGACATGATCGCCCTCATGAGCTGAGTTCAGTTCCTCCACTCTCTCTCA 1103
 Qy 151 GlyThrValArgProLysLeuProPhePheAspGluLeuThrProAlaThrPro 170
 Db 1104 GGCACAGTCAGGCCCATCTGTGCTCTCTTGTGATGAGGAGCTCACTCCAGCCACCCCA 1163
 Qy 171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu 190
 Db 1164 CTCTGGATCATGTGATGGGCTTTACGAAGCAGATGGAGGAGAGATGCTTGACATATCTG 1223
 Qy 191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaThrGln 210
 Db 1224 CTGCAGGGCTCAGTCCAGTTCATTCAGACAGCACAGGTCATGACAGCGATGCGTACCAG 1283
 Qy 211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 230
 Db 1284 GGGGAAGTACCCGAGAAGATGATGTGTGAGGATCCCGAAGGGGTGTGGACACCTGC 1343
 Qy 231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 250
 Db 1344 CAGGTGACAGTGTGGGCCCTCATGATPACCAATCTGACCAAGTGGCATGTGGTGGGATC 1403
 Qy 251 ValSerTrpGlyTyrGlyCysGlyProSerThrProGlyValTyrThrLysValSer 270
 Db 1404 GTTAGCTGGGCTATGGCTGGGGGGCCGAGCAGCCCGAGGATATACACCAAGGTCTCA 1463
 Qy 271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
 Db 1464 GCCTATCTCAACTGATCTACATGCTCTGGAAGGCTGAGCTG 1505

RESULT 9

US-10-187-749-329
 ; Sequence 329, Application US/10187749
 ; Publication No. US20030153036A1
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C1
 ; CURRENT APPLICATION NUMBER: US/10/187,749
 ; CURRENT FILING DATE: 2002-07-01
 ; PRIOR APPLICATION NUMBER: US/10/052,586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 329
 ; LENGTH: 2063
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-187-749-329

Alignment Scores:

Pred. No.: 1,67e-152 Length: 2063
 Score: 1266.00 Matches: 228
 Percent Similarity: 98.29% Conservative: 2
 Best Local Similarity: 97.44% Mismatches: 4
 Query Match: 79.12% Indels: 0
 DB: 12 Gaps: 0

US-09-607-745-9 (1-292) x US-10-187-749-329 (1-2063)

Qy 51 LysileValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
 Db 804 CGTGTGTGGTGGGGAGGAGGCTCTGTGGATTCTTGGCTTGGCAGGTGAGTCAGATCCAG 863
 Qy 71 TyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAla 90
 Db 864 TAGACAAACAGACAGCTCTGTGGAGGAGGATCTTGACCCCTTGGTCTGGTCTCAGCGCA 923
 Qy 91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
 Db 924 GCCCACTGCTTCAGAAACATACCGATGTGTCACTGGAAGTGGCGGAGGCTCAGAC 983
 Qy 111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 130
 Db 984 AAATGGGACGCTCCATCCCTGGCTGTGGCAGAGATCATCATGATGATCAATCAACCCC 1043
 Qy 131 MetTyrProLysAspAsnAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
 Db 1044 ATGTACCCCAAGACATGATCGCCCTCATGAGCTGAGTTCAGTTCCTCCACTCTCTCTCA 1103

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Qy 151 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 170
Db 1104 GGCACAGTCAGGCCCATCTGCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1163
Qy 171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 190
Db 1164 CTCTGGATCATTTGATGGGCTTTACGAAAGCAGAGATGAGGGAAGATGCTCTGACATCTG 1223
Qy 191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTy-cIln 210
Db 1224 CTGACGGCGTCAGTCCAGCTCATTCACAGCACACGTCGATGACAGATGCGATGCGTACAG 1283
Qy 211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 230
Db 1284 GGGGAAGTCACCGAGAAGATGATGTGTCAGGATCCCGGAAGGGGTGTGACACCTGC 1343
Qy 231 GlnGlyAspSerGlyGlyProLeuMetTyrglnSerAspGlnTrpHisValValGlyIle 250
Db 1344 CAGGGTGACATGATGGGCGCCCTGATGTACCAATCTGACCAAGTGGCATGTGGTGGCATC 1403
Qy 251 ValSerTrpGlyTyrglyCysGlyGlyProSerThrProGlyValTyThrLysValSer 270
Db 1404 GTTAGCTGGGCTATGGCTGGGGGCGCCGAGCACCCGAGGATATACCAAGTCTCA 1463
Qy 271 AlaTyrlLeuAsnTrpIleTyrlAsnValTrpLysAlaGluLeu 284
Db 1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505

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RESULT 10

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US-10-194-457-329
; Sequence 329, Application US/10194457
; Publication No. US20030153037A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C296
; CURRENT APPLICATION NUMBER: US/10/194,457
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 329

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; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-194-457-329

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Alignment Scores:

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Pred. No.: 1,67e-152 Length: 2063
Score: 1266.00 Matches: 228
Percent Similarity: 98.29% Conservative: 2
Best Local Similarity: 97.44% Mismatches: 4
Query Match: 79.12% Indels: 0
DB: 12 Gaps: 0

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US-09-607-745-9 (1-292) x US-10-194-457-329 (1-2063)
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Qy 51 LysIleValGlyGlyTyrlAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
Db 804 CGTGTGTGGTGGGAGGAGGCGCTCTGTGGATCTTTGGCTTGGCAGGTGAGCATCCAG 863
Qy 71 TyrlAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
Db 864 TAGACAAACAGCACGCTCTGTGGAGGAGCATCTCTGACCCCACTGGGTCTTCACGGCA 923
Qy 91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
Db 924 GCCCACTGTTCAGGAAACATACCGATGTCTCAACTGGAAGGTGCGGGCAGGCTCAGAC 983
Qy 111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 130
Db 984 AAACCTGGGAGCTTCCCATCCCTGGCTGTGGCAAGATCATCATCATGAATCAACCCC 1043
Qy 131 MetTyrlProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
Db 1044 ATGTACCCCAAGACATGACATGGCCCTCATGAAGTGCAGTTCACACTCCTTTCTCA 1103
Qy 151 GlyThrValArgProIleCysLeuProPheAspGlnGluLeuThrProAlaThrPro 170
Db 1104 GGCACAGTCAGGCCCATCTCTGTGCCCTTCTTTGATGAGGAGTCACTCCAGCCACCCCA 1163
Qy 171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 190
Db 1164 CTCTGGATCATTTGATGGGCTTTACGAACAGATGAGGGAAGATGCTCTGACATCTG 1223
Qy 191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrlGln 210
Db 1224 CTGCAGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACAG 1283
Qy 211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 230
Db 1284 GGGGAAGTCACCGAGAAGATGATGTGTCAGGATCCCGGAAGGGGTGTGACACCTGC 1343
Qy 231 GlnGlyAspSerGlyGlyProLeuMetTyrglnSerAspGlnTrpHisValValGlyIle 250
Db 1344 CAGGGTGACAGTGGTGGGCGCCCTGATGTACCAATCTGACCAAGTGGCATGTGGTGGCATC 1403
Qy 251 ValSerTrpGlyTyrglyCysGlyGlyProSerThrProGlyValTyThrLysValSer 270
Db 1404 GTTAGCTGGGCTATGGCTGGGGGCGCCGAGCACCCGAGGATATACCAAGTCTCA 1463
Qy 271 AlaTyrlLeuAsnTrpIleTyrlAsnValTrpLysAlaGluLeu 284
Db 1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505

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RESULT 11

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US-10-184-642-329
; Sequence 329, Application US/10184642
; Publication No. US20030157635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

```
/ APPLICANT: Gurney,Austin L.
/ APPLICANT: Pan,James
/ APPLICANT: Smith,Victoria
/ APPLICANT: Watanabe,Colin K.
/ APPLICANT: Wood,William I.
/ APPLICANT: Zhang,Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C194
/ CURRENT APPLICATION NUMBER: US/10/184,642
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 329
/ LENGTH: 2063
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-184-642-329

Alignment Scores:
Pred. No.: 1,67e-152 Length: 2063
Score: 1266.00 Matches: 228
Percent Similarity: 98.29% Conservative: 2
Best Local Similarity: 97.44% Mismatches: 4
Query Match: 79.12% Indels: 0
DB: 12 Gaps: 0

US-09-607-745-9 (1-292) x US-10-184-642-329 (1-2063)
QY 51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
Db 804 CGTGTGGTGGTGGGAGGAGGCTCTGTGGATCTTGGCTTGGCAGGTGAGCATCCAG 863
QY 71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
Db 864 TAGCACAAACAGACAGCTGTGGAGGAGGAGCATCTGGACCCCATCGGTCTCACGGCA 923
QY 91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
Db 924 GCCCACTGCTTCAGGAACATACCGATGTGTCAACTGGAAGGTGCGGGCAGGCTCAGAC 983
QY 111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 130
Db 984 AAACCTGGGAGCTTCCCATCCCTGGCTGTGGCAGAGATCATCATGATTAATCAACCCC 1043
QY 131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
Db 1044 ATGTACCCCAAGACATGATGCTGCTGCTTCTTTGATGAGGAGCTCATCTCCACTCTCTCA 1103
QY 151 GlyThrValArgProIleCysLeuProPheAspGluGluLeuThrProAlaThrPro 170
Db 1104 GGCACAGTCAGGCCCATCTGTCTGCCCTCTTTGATGAGGAGCTCATCTCCAGCCACCCCA 1163
QY 171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu 190
Db 1164 CTCTGGATCATTGGATGGGCTTTACGAAGCAGATGAGGAGGAGATGCTGACACTACTG 1223
QY 191 LeuGlnAlaSerValGlnValIleAspSerThrAtcCysAsnAlaAspAspAlaTyrGln 210
Db 1404 GTTAGCTGGGGCTATGCTGCGGGGGCCCGAGCAGCAGGAGGATATACACCAAGTCTCA 1463
```

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QY 271 AlaTyrLeuAsnTrpIleTyrAsnValTTrpLysAlaGluLeu 284
Db 1464 GCTATCTCACTGGATCTACAAATGCTGGAAGGCTGAGCTG 1505

RESULT 12
US-10-196-747-329
/ Sequence 329, Application US/10196747
/ Publication No. US20030162250A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C346
/ CURRENT APPLICATION NUMBER: US/10/196,747
/ CURRENT FILING DATE: 2002-07-16
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 329
/ LENGTH: 2063
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-196-747-329

Alignment Scores:
Pred. No.: 1,67e-152 Length: 2063
Score: 1266.00 Matches: 228
Percent Similarity: 98.29% Conservative: 2
Best Local Similarity: 97.44% Mismatches: 4
Query Match: 79.12% Indels: 0
DB: 12 Gaps: 0

US-09-607-745-9 (1-292) x US-10-196-747-329 (1-2063)
QY 51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
Db 804 CGTGTGGTGGTGGGAGGAGGCTCTGTGGATCTTGGCTTGGCAGGTGAGCATCCAG 863
QY 71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
Db 864 TAGCACAAACAGACAGCTGTGGAGGAGGAGCATCTGGACCCCATCGGTCTCACGGCA 923
QY 91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
Db 924 GCCCACTGCTTCAGGAACATACCGATGTGTCAACTGGAAGGTGCGGGCAGGCTCAGAC 983
QY 111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 130
Db 984 AAACCTGGGAGCTTCCCATCCCTGGCTGTGGCAGAGATCATCATGATTAATCAACCCC 1043
QY 131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
Db 1044 ATGTACCCCAAGACATGATGCTGCTGCTTCTTTGATGAGGAGCTCATCTCCACTCTCTCA 1103
QY 151 GlyThrValArgProIleCysLeuProPheAspGluGluLeuThrProAlaThrPro 170
Db 1104 GGCACAGTCAGGCCCATCTGTCTGCCCTCTTTGATGAGGAGCTCATCTCCAGCCACCCCA 1163
QY 171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu 190
Db 1164 CTCTGGATCATTGGATGGGCTTTACGAAGCAGATGAGGAGGAGATGCTGACACTACTG 1223
QY 191 LeuGlnAlaSerValGlnValIleAspSerThrAtcCysAsnAlaAspAspAlaTyrGln 210
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Db 1224 CTGACGGCTAGTCCAGGTCTATTGACAGCACACGGTGCATGACAGCATGCGTACCGAG 1283
Qy 211 GlyGluValThrGluLysMetMetCysAlaGlyValProGluGlyGlyValAspThrCys 230
Db 1284 GGGGAAGTACCGAGAGATGATGTGTGAGCATCCCGAAGGGGGTGTGACACCTGC 1343
Qy 231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyTle 250
Db 1344 CAGGGTGAAGTGTGGGGCCCTGATGTACCAATCTGACCACTGGCATGTGTGGGCATC 1403
Qy 251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
Db 1404 GTTACTGGGGCTATGGCTGGGGGGCCCGAGCACCCCGAGGAGTATACACCAAGGTCTCA 1463
Qy 271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
Db 1464 GCCTATCTCACTGGATCTACATGTCTGGAAGGCTGAGCTG 1505

RESULT 13

US-10-015-392A-274
; Sequence 274, Application US/10015392A
; Publication No. US20030166901A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C58
; CURRENT APPLICATION NUMBER: US/10/015,392A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 274
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-392A-274

Alignment Scores:

Pred. No.: 1.67e-152 Length: 2063
Score: 1266.00 Matches: 228

Percent Similarity: 98.29% Conservative: 2
Best Local Similarity: 97.44% Mismatches: 4
Query Match: 79.12% Indels: 0
DB: 12 Gaps: 0

US-09-607-745-9 (1-292) x US-10-015-392A-274 (1-2063)

Qy 51 LysIleValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
Db 804 CGTGTGGTGGGTGGGGAGAGGCGCTCTGTGTGATTCITGGCTTGGCAGTGCAGTCCAG 863
Qy 71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90
Db 864 TACGACAAACAGACAGCTCTGTGGAGGAGGATCTCTGGACCCCTGGTGGTCTCCAGGCA 923
Qy 91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
Db 924 GCCCACTGCTTCAGAAACATACCGATGTGTCACTGGAAGGTGCGGCGAGGCTCAGAC 983
Qy 111 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 130
Db 984 AACTGGGCGAGCTTCCCATCCCTGGCTGTGGCCCAAGATCATCATCATTCATTCCTCA 1043
Qy 131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
Db 1044 ATGTACCCCAAGACATGACATGCCCTCATGAGCTGCGAGTCCCACTCCACTCTCTCA 1103
Qy 151 GlyThrValArgProIleCysLeuProPhePheAspGluLeuThrProAlaThrPro 170
Db 1104 GGCACAGTCAAGGCCCATCTGTCTGCCCTCTTTGATGAGGAGCTCACTCCAGCCACCCA 1163
Qy 171 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 190
Db 1164 CTCTGGATCATTTGGATGGGCTTTACGAGCAGCAATGGAGGAGAGTGTCTGACATCTG 1223
Qy 191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrGln 210
Db 1224 CTGACGGCTGAGTCCAGGTCAATGACAGCACACGGTGCATGACAGAGTGCCTACCGAG 1283
Qy 211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 230
Db 1284 GGGGAAGTCAACGAGAGATGATGTGTGAGGATCCCGAAGGGGGTGTGACACCTGC 1343
Qy 231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyTle 250
Db 1344 CAGGGTGAAGTGTGGGGCCCTGATGTACCAATCTGACCACTGGCATGTGTGGGCATC 1403
Qy 251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
Db 1404 GTTACTGGGGCTATGGCTGGGGGGCCCGAGCACCCCGAGGAGTATACACCAAGGTCTCA 1463
Qy 271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
Db 1464 GCCTATCTCACTGGATCTACATGTCTGGAAGGCTGAGCTG 1505

RESULT 14

US-10-017-253A-274
; Sequence 274, Application US/10017253A
; Publication No. US20030166055A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James

/ APPLICANT: Paoni, Nicholas F.
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 / FILE REFERENCE: P2830P1662
 / CURRENT APPLICATION NUMBER: US/10/017,253A
 / CURRENT FILING DATE: 2001-12-13
 / PRIOR APPLICATION NUMBER: 60/098716
 / PRIOR FILING DATE: 1998-09-01
 / PRIOR APPLICATION NUMBER: 60/098723
 / PRIOR FILING DATE: 1998-09-01
 / PRIOR APPLICATION NUMBER: 60/098749
 / PRIOR FILING DATE: 1998-09-01
 / PRIOR APPLICATION NUMBER: 60/098750
 / PRIOR FILING DATE: 1998-09-01
 / PRIOR APPLICATION NUMBER: 60/098803
 / PRIOR FILING DATE: 1998-09-02
 / PRIOR APPLICATION NUMBER: 60/098821
 / PRIOR FILING DATE: 1998-09-02
 / PRIOR APPLICATION NUMBER: 60/098843
 / PRIOR FILING DATE: 1998-09-02
 / PRIOR APPLICATION NUMBER: 60/099536
 / PRIOR FILING DATE: 1998-09-09
 / PRIOR APPLICATION NUMBER: 60/099596
 / PRIOR FILING DATE: 1998-09-09
 / PRIOR APPLICATION NUMBER: 60/099598
 / PRIOR FILING DATE: 1998-09-09
 / Remaining Prior Application data removed - See File Wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 477
 / SEQ ID NO 274
 / LENGTH: 2063
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / US-10-017-253A-274

Alignment Scores:

Pred. No.:	1.67e-152	Length:	2063
Score:	1266.00	Matches:	228
Percent Similarity:	98.29%	Conservative:	2
Best Local Similarity:	97.44%	Mismatches:	4
Query Match:	79.12%	Indels:	0
DB:	12	Gaps:	0

US-09-607-745-9 (1-292) x US-10-017-253A-274 (1-2063)

QY	51	LysileValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln	70
DB	804	CGTGTGTGGTGGGAGGAGGCTCTGTGGATTCTTGGCTTGGCAGGTCAGCATCCAG	863
QY	71	TyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAla	90
DB	864	TACGACAAACAGCAGCTGTGGAGGAGCATCTTGACCCCACTGGTCTTCCACGGCA	923
QY	91	AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp	110
DB	924	GCCCACTGCTTCAGAAACATACCGATGTGTCACTGGAAGGTGCGGAGGCTCAGAC	983
QY	111	LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro	130
DB	984	AACTGGGAGCTTCCCATCCCTGGCTGTGGCCCAAGATCATCAATGATTAATCAACCCC	1043
QY	131	MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer	150
DB	1044	ATGTACCCCAAGACATGATCGCTCATGAGGTGAGTTCACACTTCATCTTCTCA	1103
QY	151	GlyThrValArgProIleCysLeuProPhePheAspGluLeuThrProAlaThrPro	170
DB	1104	GGCACAGTCAGGCCCACTGTCTGCCCTCTTTGATGAGGAGCTCACTCCAGCCACCCCA	1163
QY	171	LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu	190
DB	1164	CTCTGGATCATTTGATGGGCTTTTACGAAGCAGATGAGGAAAGATGTCTGACATATG	1223
QY	191	LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrGln	210

DB	1224	CTGCAGGCTCAGTCAGTCCATTTGCACACACGGTCAATGCACAGCATGGTACACG	1283
QY	211	GlyGluValThrGlnLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys	230
DB	1284	GGGAAAGTCACCGAGAAGATGATGTGTGAGGATCCCGAGGGGTGTGGACACTGC	1343
QY	231	GlnGlyAspSerGlyClyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle	250
DB	1344	CAGGGTGACAGTGGTGGCCCTGATGTACCAATCTGCACAGTGGCATGTGGTGGGCATC	1403
QY	251	ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer	270
DB	1404	GTTAGCTGGGGCTATGGCTGGGGGGCCCGAGCACCCCGAGGATATACCAAGGCTCA	1463
QY	271	AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu	284
DB	1464	GCCTATCTCAACTGGATCTTACAATGTCTGGAAGGCTGAGCTG	1505

RESULT 15

US-10-173-689-329
 ; Sequence 329, Application US/10173689
 ; Publication No. US20030166104A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C10
 ; CURRENT APPLICATION NUMBER: US/10/173,689
 ; CURRENT FILING DATE: 2002-06-17
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 329
 ; LENGTH: 2063
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-173-689-329

Alignment Scores:

Pred. No.:	1.67e-152	Length:	2063
Score:	1266.00	Matches:	228
Percent Similarity:	98.29%	Conservative:	2
Best Local Similarity:	97.44%	Mismatches:	4
Query Match:	79.12%	Indels:	0
DB:	12	Gaps:	0

US-09-607-745-9 (1-292) x US-10-173-689-329 (1-2063)

QY	51	LysileValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln	70
DB	804	CGTGTGTGGTGGGAGGAGGCTCTGTGGATTCTTGGCTTGGCAGGTCAGCATCCAG	863
QY	71	TyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAla	90
DB	864	TACGACAAACAGCAGCTGTGGAGGAGCATCTTGACCCCACTGGTCTTCCACGGCA	923
QY	91	AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp	110
DB	924	GCCCACTGCTTCAGAAACATACCGATGTGTCACTGGAAGGTGCGGAGGCTCAGAC	983
QY	111	LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro	130
DB	984	AACTGGGAGCTTCCCATCCCTGGCTGTGGCCCAAGATCATCAATGATTAATCAACCCC	1043

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Qy 131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
Db 1044 ATGTACCCCAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCA 1103
Qy 151 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 170
Db 1104 GGCACAGTCAGGCCCATCTGCTGCGCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1163
Qy 171 LeuTyrPileIleGlyThrGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 190
Db 1164 CTCGGATCATTTGGATGGGCTTTACGAAGCAGAAATGGAGGAGAGATCTCGACATACTG 1223
Qy 191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrGln 210
Db 1224 CTGCAGGGGTCACTCCAGGTCAATTGACAGCACACGGTGCATGCAGACGATGCGTACCAG 1283
Qy 211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 230
Db 1284 GGGGAAGTCACCGAAGATGATGTGTGCAGGCATCCCGAAGGGGGTGTGCACACCTGC 1343
Qy 231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTyrHisValValGlyIle 250
Db 1344 CAGGTGCACGTGTGGGCCCTGTATGTACCAATCTGCCAGTGGCAITGTGTGGGCATC 1403
Qy 251 ValSerTyrGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
Db 1404 GTTAGCTGGGGCTATGGCTGGGGGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCA 1463
Qy 271 AlaTyrLeuAsnTyrPileTyrAsnValTyrPylsAlaGluLeu 284
Db 1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505
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Search completed: December 2, 2003, 05:05:22
Job time : 275.18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 2, 2003, 02:30:15 ; Search time 56.2311 Seconds
(without alignments)
2292.040 Million cell updates/sec

Title: US-09-607-745-9

Perfect score: 1500

Sequence: 1 MDSKGSQSKRLLLLVSN.....LNWYNVWKAELGRHHHHH 292

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued Patents NA -QFWT=fastap -SUFFIX=tni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1266	79.1	2038	3	US-09-008-271A-18
2	1266	79.1	2079	4	US-09-656-002-1
3	765	47.8	1130	4	US-09-387-375-8
4	754.5	47.2	1130	4	US-09-386-553A-8
5	746	46.6	1169	4	US-09-386-642-7
6	740.5	46.3	1166	4	US-09-386-629-2
7	672.5	42.0	1052	4	US-09-386-642-10
8	645	40.3	1049	4	US-09-386-642-9
9	601.5	37.6	1103	4	US-09-386-642-59
10	593	37.1	1142	4	US-09-386-642-8
11	574	35.9	1037	4	US-09-386-642-60
12	526.5	32.9	1460	4	US-09-370-838-80

13	526.5	32.9	1517	1	US-08-508-448C-15	Sequence 15, Appl
14	526.5	32.9	2790	4	US-09-370-838-79	Sequence 79, Appl
15	524.5	32.8	1462	4	US-09-370-838-55	Sequence 55, Appl
16	522.5	32.7	696	1	US-08-508-448C-24	Sequence 24, Appl
17	510.5	31.9	901	1	US-08-508-448C-9	Sequence 9, Appl
18	508	31.8	2479	3	US-09-342-749-29	Sequence 29, Appl
19	508	31.8	2479	4	US-09-691-840-29	Sequence 29, Appl
20	506	31.6	1479	3	US-09-342-749-1	Sequence 1, Appl
21	506	31.6	1479	4	US-09-691-840-1	Sequence 1, Appl
22	505.5	31.6	1615	4	US-09-820-002-1	Sequence 1, Appl
23	505.5	31.6	1783	3	US-09-510-738A-188	Sequence 188, App
24	505.5	31.6	1783	4	US-09-861-966-188	Sequence 188, App
25	505.5	31.6	2363	4	US-09-742-703-3	Sequence 3, Appli
26	502	31.4	2413	3	US-09-518-046-1	Sequence 1, Appli
27	497	31.1	1077	3	US-08-807-151-2	Sequence 2, Appli
28	497	31.1	1077	4	US-09-478-957-2	Sequence 2, Appli
29	491.5	30.7	1605	2	US-09-000-846-1	Sequence 1, Appli
30	482	30.1	959	4	US-09-023-942A-25	Sequence 25, Appl
31	478.5	29.9	2544	3	US-09-518-046-3	Sequence 3, Appli
32	473	29.6	2416	3	US-09-261-416-1	Sequence 1, Appli
33	456.5	28.5	1100	4	US-09-023-942A-5	Sequence 5, Appli
34	455	28.4	1613	4	US-09-387-375-1	Sequence 1, Appli
35	453.5	28.3	897	2	US-08-956-267A-1	Sequence 1, Appli
36	451.5	28.2	1081	3	US-09-008-271A-15	Sequence 15, Appl
37	450.5	28.2	1094	4	US-09-023-942A-3	Sequence 3, Appli
38	444	27.8	3147	2	US-09-027-337-1	Sequence 1, Appli
39	444	27.8	3147	4	US-09-644-600-1	Sequence 1, Appli
40	444	27.8	3147	4	US-09-644-600-18	Sequence 18, Appl
41	443.5	27.7	825	3	US-09-120-582-1	Sequence 1, Appli
42	442.5	27.7	980	4	US-09-023-942A-30	Sequence 30, Appl
43	442.5	27.7	1110	4	US-09-386-653A-1	Sequence 1, Appli
44	437.5	27.3	1212	4	US-09-620-312D-431	Sequence 431, App
45	431.5	27.0	1225	4	US-09-734-675-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-008-271A-18
; Sequence 18, Application US/09008271A
; Patent No. 6203979

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; Hillman, Jennifer L.

; Yue, Henry

; Guegler, Karl J.

; Corley, Neil C.

; Tang, Tom Y.

; Shah, Purvi

; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/008,271A

; FILING DATE: 16-Jan-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: <Unknown>

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Mohan-Peterson, Sheela

; REGISTRATION NUMBER: 41,201

; REFERENCE/DOCKET NUMBER: PF-0458 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-853-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLNOT13
CLONE: 1337018
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-008-271A-18

Alignment Scores:
Pred. No.: 5,58e-130 Length: 2038
Score: 1266.00 Matches: 228
Percent Similarity: 98.29% Conservative: 2
Best Local Similarity: 97.44% Mismatches: 4
Query Match: 79.12% Indels: 0
DB: 3 Gaps: 0

US-09-607-745-9 (1-292) x US-09-008-271A-18 (1-2038)

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Db 803 CGTGTGGTGGTGGGAGGAGGCTCTGTGGATCTTGGCTTGGCAGGTGAGCATCCAG 862
Qy 71 TyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAla 90
Db 863 TAGGACAAACAGCAGCTGTGGAGGAGCARTCTGGACCCCACTGGTCTCCTCAGGCA 922
Qy 91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
Db 923 GCCCACTGCTTCAGAAACATACCATGTGTCACTGGAGAGTGGCGGAGGCTCAGAC 982
Qy 111 LysLeuGlySerPheProSerLeuAlaValAlaLysIlellellelleGluPheAsnPro 130
Db 993 AAACCTGGGACGTTCCCACTCCCTGTGCTGTGGCAAGATCATCATTAATCAACCCC 1042
Qy 131 MetTyrProLysAspAsnAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
Db 1043 ATGTACCCCAAGACATGACATCCCTCATGAAGCTGCAGTTCCTCCACTCACATTCTCA 1102
Qy 151 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 170
Db 1103 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGTCACTCCAGCCACCCA 1162
Qy 171 LeuTrpIlellelleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu 190
Db 1163 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGATGAGGAGGAGATGCTGACATACGT 1222
Qy 191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrlGln 210
Db 1223 CTGAGGGGCTGATCCAGGTATTCAGACACACCGTGCATGACAGAGTGGCGTACCCAG 1282
Qy 211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 230
Db 1283 GGGGAAGTCACCGAAGATGATGTGTGAGGATCCCGAAGGGGGGTGGACACCTGTC 1342
Qy 231 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 250
Db 1343 CAGGTGACAGTGGTGGGCCCCCTGATGATGACCAATCTGACCATGTCAGTGGCATGTGGTGGCATC 1402
Qy 251 ValSerTrpGlyTyTrGlyCysGlyGlyProSerThrProGlyValTyThrLysValSer 270
Db 1403 GTTAGTGGGCTATGGCTGGGGGGCCCCGAGCACCCCGAGGAGTATACCAAGGTCTCA 1462
Qy 271 AlaTyrLeuAsnTrpIleTyAsnValTrpLysAlaGluLeu 284
Db 1463 GCCTATCTCAACTGGATCTACATGTCTGGAAGGCTGAGCTG 1504

RESULT 2

US-09-656-002-1
Sequence 1, Application US/09656002
Patent No. 6455668
GENERAL INFORMATION:
APPLICANT: Mack, David
APPLICANT: Gish, Kurt
APPLICANT: Wilson, Keith
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
FILE REFERENCE: A-69108/DJB/JUD/AMS
CURRENT FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: US 09/656,002
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 09/525,993
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 09/493,444
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: PCT/US 00/07044
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 2079
TYPE: DNA
ORGANISM: Homo sapiens
US-09-656-002-1
Alignment Scores:
Pred. No.: 5,74e-130 Length: 2079
Score: 1266.00 Matches: 228
Percent Similarity: 98.29% Conservative: 2
Best Local Similarity: 97.44% Mismatches: 4
Query Match: 79.12% Indels: 0
DB: 4 Gaps: 0
US-09-607-745-9 (1-292) x US-09-656-002-1 (1-2079)

Qy 51 LysleValGlyGlyTyAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln 70
Db 818 CGTGTGGTGGTGGGAGGAGGCTCTGTGGATCTTGGCTTGGCAGGTGAGCATCCAG 877
Qy 71 TyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAla 90
Db 878 TAGACAAACAGCAGCTGTGGAGGAGCATCTCTGGACCCCACTGGTCTCCTCAGGCA 937
Qy 91 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 110
Db 938 GCCCACTGCTTCAGAAACATACCGATGTGTCACTGGAGAGTGGCGGAGGCTCAGAC 997
Qy 111 LysLeuGlySerPheProSerLeuAlaValAlaLysIlellellelleGluPheAsnPro 130
Db 998 AAACCTGGGACGTTCCCACTCCCTGTGCTGTGGCAAGATCATCATTAATCAACCCC 1057
Qy 131 MetTyrProLysAspAsnAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
Db 1058 ATGTACCCCAAGACATGACATCGCCCTCATGAAGCTGAGTTCACACTCACATTCTCA 1117
Qy 151 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 170
Db 1118 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGTCACTCCAGCCACCCA 1177
Qy 171 LeuTrpIlellelleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu 190
Db 1178 CTCTGGATCATTGGATGGGGCTTTACGAAGCAGATGAGGAGGAGATGTCTGACATACGT 1237
Qy 191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrlGln 210
Db 1238 CTGAGGGGCTGATCCAGGTATTCAGACACACCGTGCATGACAGATGTCGATACCCAG 1297
Qy 211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 230
Db 1298 GGGGAAGTCACCGAAGATGATGTGTGAGGAGTATCCCGAAGGGGTGGACACCTGTC 1357

US-09-607-745-9 (1-292) x US-09-386-653A-8 (1-1130)

```
Qy 1 MetAspSerLysGlySerSerGlnLysSerArgLeuLeuValValSerAsn 20
Db 13 ATGACAGCAAGGTTCTCGCAGAAATCCGCCCTCTCTGCTGGTGTCAAAAT 72
Qy 21 LeuLeuLeuCysGlnGlyValValSerAspTyrLysAspAspValAlaAla 40
Db 73 CTACTCTTGTCAGGGTGTCTCCGACTACAGGACGACGACGACGACGACG 132
Qy 41 AlaLeuAlaAlaProPheAspAspAspLysLeuValGlyTyrAlaLeuVal 60
Db 133 GCTCTTGCTGCCCTTTGATGATGATGATGATGATGATGATGATGATG 192
Qy 61 AspSerTrpProTyrGlnValSerLysGlnHisValCysGlySer 80
Db 193 GCGAGTGGCCCTCGCAGAGTTCAGCATCACCTATGAAGCGCTCCATGCT 252
Qy 81 IleLeuAspProHisTyrValValSerAlaAlaHisCysPheArgLysHis 100
Db 253 CTCATCGCGGACGACGAGTGGTCTCGACGCTGCTCCGCAACACACCTCT 312
Qy 101 PheAsnTrpLysValArgAlaGlySerLysLeu---GlySerPheProSer 119
Db 313 TCCCTGTACCAAGGTCCTGCTGGGGCAAGGACGAGTAGTCAGCGGACCA 372
Qy 120 ValAlaLysLysLysLysLysLysLysLysLysLysLysLysLysLys 136
Db 373 TATCCCGGCTGAGCGAGTGGGTCCTGACGGCTGCGACTGCTCCGCAAC 432
Qy 137 AspLeuAlaLeuMetLysLeuGlnPheProLeuThrPheSerGlyThrVal 156
Db 433 GACGTGGCCCTGGTGGAGCTGGAGCACGACGCTTCACCAATATCATCTCC 492
Qy 157 CysLeuProPheAspGluLeuThrProAlaThrProLeu-----Trp 174
Db 493 TGCCTGCTCT-----GACCCCTGGTGATCTTTGAGACGGGCATGAAT 546
Qy 175 GlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAsp----- 188
Db 547 GGCTGGGCGACCCCGAGTGAG-----GAGACCTCTCTGCGGACCGCG 591
Qy 189 IleLeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsn 204
Db 592 ATCCGTGCAAAACTCGCTGTGCCATCATCGACACACCCAAAGTGCACCTG 651
Qy 205 -----AlaAspAlaTyrGlnGlyGlu---ValThrGluLysMetCysAla 221
Db 652 AAGACACCGAGTTGGTACCAACCCAAACCATCAGAAATGACATGCTGTG 711
Qy 222 IleProGluGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMet 241
Db 712 TTCAGGAGGCAAGAGAGTGCCTCAAGGCGACTCGGCGGCCCTCGTGTG 771
Qy 242 SerAspGln---TrpHisValValGlyLysValSerTrpGlyCysGlyGly 260
Db 772 GTGGGTGAGTGTGCTGTCAGCGCGGGGTGATCAGCTGGGTGAGGGTGTG 831
Qy 261 SerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyr 279
Db 832 AACCGCCAGGTGTCTACATCGGTGTACCCGCCCAACCACTGGATTCATCG 891
Qy 280 -----TrpLysAlaGluLeuSerArgHisHisHis 290
Db 892 CCCAACTGCAGTTCCAGCCAGCGAGGTGGCGGCGCCAGAGTCTAGACAT 951
Qy 291 HisHis 292
Db 952 CATCAC 957
```

RESULT 5

US-09-386-642-7

; Sequence 7, Application US/09386642

```
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: OST-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1169
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-7

Alignment Scores:
Pred. No.: 5,83e-73 Length: 1169
Score: 746.00 Matches: 163
Percent Similarity: 60.37% Conservative: 35
Best Local Similarity: 49.70% Mismatches: 94
Query Match: 46.62% Indels: 36
DB: 4 Gaps: 8

US-09-607-745-9 (1-292) x US-09-386-642-7 (1-1169)
Qy 1 MetAspSerLysGlySerSerGlnLysSerArgLeuLeuValValSerAsn 20
Db 13 ATGACAGCAAGGTTCTCGCAGAAATCCGCCCTCTCTGCTGGTGTCAAAAT 72
Qy 21 LeuLeuLeuCysGlnGlyValValSerAspTyrLysAspAspValAlaAla 40
Db 73 CTACTCTTGTCAGGGTGTCTCCGACTACAGGACGACGACGACGACGACG 132
Qy 41 AlaLeuAlaAlaProPheAspAspAspLysLeuValGlyTyrAlaLeuVal 60
Db 133 GCTCTTGCTGCCCTTTGATGATGATGATGATGATGATGATGATGATG 192
Qy 61 AspSerTrpProTyrGlnValSerLysGlnHisValCysGlyGlySer 80
Db 193 GGTGAGTGGCCCTCGCAGAGTTCAGCATCACCTATGAAGCGCTCCATGCT 252
Qy 81 IleLeuAspProHisTyrValValSerAlaAlaHisCysPheArgLysHis 100
Db 253 CTCGTGTCTGAGCAGTGGGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 312
Qy 101 PheAsnTrpLysValArgAlaGlySerAspLysLeuGlySerPheProSer 119
Db 313 GAAGCCTATGAGTCAAGTGGGGGCCACCCAGCTTACCTCCGAGGAGGCT 372
Qy 120 ValAlaLysLysLysLysLysLysLysLysLysLysLysLysLysLys 136
Db 373 GTGACACCCCTGAAGACATCATCCCCACCCAGCTTACCTCCGAGGAGG 432
Qy 137 AspLeuAlaLeuMetLysLeuGlnPheProLeuThrPheSerGlyThrVal 156
Db 433 GACATTGCACTCTCCAACTCAGACACCATCACCTTCTCCGCTACATCCG 492
Qy 157 CysLeuProPheAspGluLeuThrProAlaThrProLeuTrpIleLeuGly 176
Db 493 TGCTCTCCCTGCACCAACGCTCTCTCCCAACGGCTCCACTGCTGCTGG 552
Qy 177 GlyPheThrLysGlnAsnGlyGlyLysMetSer---AspIleLeuLeu 195
Db 553 GGTCAATGTGGCCCCCTCAGTGAGCCCTCTGACGCCCAAGCCACTGCA 612
Qy 196 GlnValIleAspSerThrArgCysAsnAla-----AspAlaTyrGln 212
Db 613 CCTCTGATCAGTGTGAGACGTTGTAATCTGCTGTACAAATCGACGCA 672
```

QY 213 -----ValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThr 229
 Db 673 CCGACATTGTCGAAGAGGACATGTTGCTGCTGCTATGTGGAGGGGGGCAAGAGGCC 732
 QY 230 CysGlnGlyAspSerGlyProLeuMetTyrglnSerAsp---GlnTrpHisValVal 248
 Db 733 TGCCAGGGTGACTCTGGGGGCCCACTCTCTGCCCTGTGGAGGGTCTCTGGTACTCAGC 792
 QY 249 GlyIleValSerTrpGlyTyrglyCysGlyGlyProSerThrProGlyValTyrrlys 268
 Db 793 GGCATTGTGAGCTGGGAGATGCTGTGGGGCCGCAACAGCCCTGTGTGTACACTCTG 852
 QY 269 ValSerAlaTyrrLeuAsnTrpIleTyrr----- 277
 Db 853 GCCTCCAGCTATGCTCTCTGATCCAAAGCAAGTGAGTGACAGACTCCAGCCTCGTGTGGTG 912
 QY 278 -----AsnValTrpLysAlaGluLeu----- 284
 Db 913 CCCCACAAACCCAGGAGTCCAGCCGACAGCAACCTCTGTGGCAGCCACCTGGCCTTCAGC 972
 QY 285 SerArgHisHisHisHisHis 292
 Db 973 TCTAGACATCACCATCACCATCAC 996

RESULT 6

US-09-386-629-2
 ; Sequence 2, Application US/09386629
 ; Patent No. 6426199
 ; GENERAL INFORMATION:
 ; APPLICANT: Darrow, Andrew L.
 ; APPLICANT: Qi, Jensen
 ; APPLICANT: Andrade-Gordon, Patricia
 ; TITLE OF INVENTION: Identification and Characterization of the complementary
 ; FILE REFERENCE: ORT-1030
 ; CURRENT APPLICATION NUMBER: US/09/386,629
 ; CURRENT FILING DATE: 1999-08-31
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1166
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: C-E catalytic
 ; OTHER INFORMATION: domain in a zymogen activated construct
 US-09-386-629-2

Alignment Scores:

Pred. No.: 2,35e-72 Length: 1166
 Score: 740.50 Matches: 164
 Percent Similarity: 61.70% Conservative: 39
 Best Local Similarity: 49.85% Mismatches: 87
 Query Match: 46.28% Indels: 39
 DB: 4 Gaps: 10

US-09-607-745-9 (1-292) x US-09-386-629-2 (1-1166)

QY 1 MetAspSerLysGlySerSerGlnLysSerArgLeuLeuLeuValSerAsn 20
 Db 13 ATGCACAGCAAGGTTCTGTCGCAAAATCCGCTGTCTCTGCTGTGGTGTCAAT 72
 QY 21 LeuLeuLysGlnGlyValValSerAspTyrrLysAspAspValAlaAla 40
 Db 73 CTACTCTGTGCCAGGTGTGTCTCCGACTACAAAGCAGCAGCAGCGCGGCC 132
 QY 41 AlaLeuAlaAlaProPheAspAspAspLysIleValGlyTyrrAlaLeuAspVal 60
 Db 133 GCCTTCTGCCCCCTTTTGATGATGATGACAAAGATCGTTGGGGCTATGCTTAGAGGAC 192
 QY 61 AspSerTrpProTrpGlnValSerIleGlnTyrrAspLysGlnHisValCysGlyGlySer 80

Db 193 AGCAGTGGCCCTGGATCGTGACATCCAGAAATGGGACCCACCACTGGCGAGGTCT 252
 QY 81 IleLeuAspProHisTrpValLeuThrAlaAlaHisCysPheArgLysHisThrAsp--- 99
 Db 253 CTGCTCACCAGCCGCTGGGTGATCACTGTGCTGCCACTGTTCAGGAGCAACCTGAACAAA 312
 QY 100 ValPheAsnTrpLysValArgAlaGlySerAspLysLeuGlySerPheProSerLeuAla 119
 Db 313 CCATACCTGTCTCTGTGTGTGGGGGCTGCAGCTGGGGAAC---CCTGGCTCTCGG 369
 QY 120 ValAlaLysIleIleIle-----IleGluPheAsnProMetTyrrPro---LysAspAsn 136
 Db 370 TCCAGAGTGGGTGTGTCTGGGTGGAGCCCACTCTGTATTCCTCGAAGAGAGGT 429
 QY 137 -----AspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSerGlyThrVal 153
 Db 430 GCCTGTGTGCAGACATTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 489
 QY 154 ArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrProLeuTrpIle 173
 Db 490 CTGCCATCTGCTTACCTGATGCTCTATCCACTCCCTCCAAACACCCACTGCTGTGATC 549
 QY 174 IleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMet-----SerAspIleLeuLeu 191
 Db 550 TCAGGCTGGGG---AGCATCCAAGATGGAGTTCCTTGCCCACTCAGACCTCAG 606
 QY 192 GlnAlaSerValGlnValIleAspSerThrArgCysAsnAla-----AspAspAla 208
 Db 607 AAGCTGAAGGTTCTATCATCATCGACTCGGAAGTCTGCAGCCATCTGTACTGGCGGGAGCA 666
 QY 209 TyrglnGlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAsp 228
 Db 667 GGCAGGAGCCCACTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 726
 QY 229 ThrCysGlnGlyAspSerGlyGlyProLeuMetTyrrGlnSerAsp---GlnTrpHisVal 247
 Db 727 GCTGTGTGGCGACTCCGGGGGCCCCCTCATGTGCCAGTGCAGCGGCTGGTGTCTG 786
 QY 248 ValGlyIleValSerTrpGlyTyrrGlyCysGlyGlyProSerThrProGlyValTyrrThr 267
 Db 787 GCCGGCATCATCAGCTGGCGGAGGGCTGTGCCAGCGCAACAGCGCCGGGCTTACATC 846
 QY 268 LysValSerAlaTyrrLeuAsnTrpIleTyrrAsnValTrpLys----- 281
 Db 847 AGCCTCTCTGCGCACCCCTCTCTGCTGGTGGAGAGATCGTGCAGGGGTGCAGCTCCCGCGG 906
 QY 282 -----AlaGlu 283
 Db 907 CGCGCTCAGGGGGTGGGGCCCTCAGGGCACCGAGGGCTCTGGGGCGCGCGCGC 966
 QY 284 LeuSerArgHisHisHisHisHis 292
 Db 967 TCCTCTAGACATCACCATCACCATCAC 993
 RESULT 7
 ; Sequence 10, Application US/09386642
 ; Patent No. 6420157
 ; GENERAL INFORMATION:
 ; APPLICANT: Darrow, Andrew
 ; APPLICANT: Qi, Jensen
 ; APPLICANT: Andrade-Gordon, Patricia
 ; TITLE OF INVENTION: Zymogen Activation System
 ; FILE REFERENCE: ORT-1028
 ; CURRENT APPLICATION NUMBER: US/09/386,642
 ; CURRENT FILING DATE: 1999-08-31
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 1052
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
 ; OTHER INFORMATION: with homo sapien serine protease catalytic domain
 US-09-386-642-10

Alignment Scores:		
Pred. No.:	6,43e-65	Length: 1052
Score:	672.50	Matches: 148
Percent Similarity:	61.31%	Conservative: 39
Best Local Similarity:	48.52%	Mismatches: 89
Query Match:	42.03%	Indels: 29
DB:	4	Gaps: 11

US-09-607-745-9 (1-292) x US-09-386-642-10 (1-1052)

QY	1	MetAspSerLysGlySerSerGlnLysSerArgLeuLeuLeuLeuValValSerAsn	20
Db	13	ATGGACAGCAAAAGTTCTCGCAGAAATCCCGCTGCTCTGCTGTGGTGTCAAAAT	72
QY	21	LeuLeuLeuCysGlnGlyValValSerAspTyrLysAspAspAspValAspAlaAla	40
Db	73	CTACTCTGTGCCAGGTTGTCTCCGACTTCAAGGACGACGACGCGGCGGC	132
QY	41	AlaLeuAlaAlaProPheAspAspAspLysIleValGlyGlyTyr---AlaLeuAsp	59
Db	133	GCTCTGTCTGCCCTTTTGATGATGATGACAAGATCTTGGGGCTACAACTGCTCAGAA	192
QY	60	ValAspSerTrpProTrpGlnValSerIleGlnTrpAspLysGlnHisValCysGlyGly	79
Db	193	ANGACTCCGAGCCCTGGCAGCGCCCTGTCGAGAAGACGGCGGTCTCTGTGGGGC	252
QY	80	SerIleLeuAspProHisTrpValLeuThrAlaAlaHisCysPheArgLys-----	96
Db	253	ACGCTCATCGCCCCAGATGGCTCTGACACAGCCCACTGCTCAAGCCCGCTACATA	312
QY	97	---HisThrAspValPheAsnTrpLysValArgAlaGlySerAspLys-----	111
Db	313	GTTCACCTGGGGCAGCAACAATCCAGAGGAGGGCTGTGAGCAGACCCGACAGCC	372
QY	112	LeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnProMet	131
Db	373	ACTGAGTCTCTCCCCACCCCGGC-----TTCAACAACACAGC	408
QY	132	TyrPro---LysAsp-----AsnAspIleAlaLeuMetLysLeuGlnPheProLeuThr	148
Db	409	CTCCCAACAAGACACCCGCAATGACATCATGCTGTGAAGTGGCATCGCAGCTTCC	468
QY	149	PheSerGlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAla	168
Db	469	ATCACTGGGCTGTGGACCCCTCACCCTCTCC-----TCACGCTGTGTCACTGTCTGGC	522
QY	169	ThrProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAsp	188
Db	523	ACCACTGCCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCCAGATTACGCTGCCTCAC	582
QY	189	IleLeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAla	208
Db	583	ACCTTGGATGCGCCAAACATCACCATCATTGAGCACCAGAGTGT-----GAGAACGCC	636
QY	209	TyrGlnGlyGluValThrGlnLysMetMetCysAlaGlyIleProGluGlyGlyValAsp	228
Db	637	TACCCCGGCAACATCACAGACCATGTTGTGTGCCAGCTGCAGGAAGGGGGCAGGAC	696
QY	229	ThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValVal	248
Db	697	TCTGTCAGGGTGAATCCGGGGGCCCTCTGTGTTGAACAGTCT-----CTTCAA	747
QY	249	GlyIleValSerTrpGlyTyrGly---CysGlyGlyProSerThrProGlyValTyrThr	267
Db	748	GGCATTAATCTCTGGGGCAGGATCCGTTGTCGATACCCGAAAGCCTGGTGTCTACAG	807
QY	268	LysValSerAlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeuSerArgHis	287
Db	808	AAAGTCTGCAATATGTGGCTGGATCCAGAGACGATGAGAACCAATCTCTACAT	864

US-09-386-642-60

US-09-607-745-9 (1-292) x US-09-386-642-60 (1-1037)

QY 175 GlyTrpGlyPheThrLysClnAsnGlyGlyLysMetSerAspIleLeuLeuGlnAlaSer 194

[illegible]

```
Db 532 GGCTGGGGTCTGCTGGCG-----AACGGCAGAGTCTACCGTGTGCTGAGTGGTGAAC 585
Qy 195 ValGlnValIleAspSerThrArgCysAsnAla-----AspAspAlaTyrGlnGlyGlu 212
Db 586 GTGTCGGTGTGTGTGAGGAGGTCTGCAGTAAGTCTATGACCGCTGTATCCAC-----639
Qy 213 ValThrGluLysMetMetCysAlaGlyIleProGluGlyValAspThrCysGlnGly 232
Db 640 -----CCCGACATGTTCTGCGCGCGGGAGGCGACACAGAGGACTCTCTGCAACGGT 693
Qy 233 AspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIleValSer 252
Db 694 GACTCTGGGGCGCCCTGATCTGCAACGGG-----TACTTGCAGGGCGCTGTGTCT 744
Qy 253 TrpGlyTyrGly---CysGlyGlyProSerThrProGlyValTyrThrLysValSerAla 271
Db 745 TTGGGAAAGCCCGCTGTGGCCAAAGTTGGCGTGCAGGTGTCTACACCAACCTCTGCAAA 804
Qy 272 TyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeuSerArgHisHisHisHis 291
Db 805 TTCACTGAGTGGATAGAGAAACCGTCCAGGCCAGT---TCTAGACATCACCATCACCAT 861
Qy 292 His 292
Db 862 CAC 864

RESULT 12
US-09-370-838-80
; Sequence 80, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Radoch
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-370-838-80

Alignment Scores:
Pred. No.: 1.31e-48 Length: 1460
Score: 526.50 Matches: 97
Percent Similarity: 62.93% Conservative: 49
Best Local Similarity: 41.81% Mismatches: 79
Query Match: 32.91% Indels: 7
DB: 4 Gaps: 4

US-09-607-745-9 (1-292) x US-09-370-838-80 (1-1460)
Qy 49 AspAspLysIleValGlyGlyIleValAlaLeuAspValAspSerTrpTrpGlnValSer 68
Db 601 GAGCAGAGATCTTGGAGGACTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGTCAGT 660
Qy 69 IleGlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeu 88
Db 661 CTGGGGCTCAATAATGCCACCACTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Qy 89 ThrAlaAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGly 108
Db 721 ACAGCAGCTCACTGTTTCCAGAGCAACTCTAATCTGCTGAGTGTGATGCCACGCTGTT 780
Qy 109 SerAspLysLeuGlySerPheProSerLeu-----AlaValAlaLysIleIleIle 126
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Db 781 ATTTCACA-----ACATTTCCTAACTAGAAATGAGAGTAAGAAATATTTTAAATTCAT 834
Qy 127 GluPheAsnProMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPhePro 146
Db 835 AACAAATTATAAATCTCAACTCATGAAATGACATTGCACCTTGAGACTTGAGAACAGT 894
Qy 147 LeuThrPheSerGlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThr 166
Db 895 GTCACTTTTACCAAGATATCCATAGTGTGTCTCCAGCTCTACCCAGAAATATTTCCA 954
Qy 167 ProAlaThrProLeuTrpIleLeuGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMet 186
Db 955 CCTGGCTCTACTCTATGTAACAGAGTGGGGCGCTCAAGAATATGCTGCCACACAGTT 1014
Qy 187 SerAspIleLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAsp 206
Db 1015 CCAGAG---CTAAGGCAAGCAGACAGTCAAGTAATAAGTAATGATGATGTAATGCACCA 1071
Qy 207 AspAlaTyrGlnGlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGly 226
Db 1072 CATAGTATAAATGAGGCCATCTTGTCTGGAATCTGTGTGCTGGAGTACCTCAAGGTGA 1131
Qy 227 ValAspThrCysGlnGlyAspSerGlyProLeuMetTyrGlnSerAspGln-----244
Db 1132 GTGAGCGCATGTCAGGGTGACTCTGTGGGCCACTAGTACAAGAAGACTCAAGCGGCTT 1191
Qy 245 TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGly 264
Db 1192 TGGTTTATTGTGGGATAGTAGCTGGGAGATCAGTGTGGCTGCCGGATAAGCCAGGA 1251
Qy 265 ValTyrThrLysValSerAlaTyrLeuAsnTrpIle 276
Db 1252 GTGTATCTACTGAGTGACAGCCTACTGTGACTGGATT 1287

RESULT 13
US-08-508-448C-15
; Sequence 15, Application US/08508448C
; Patent No. 5804410
; GENERAL INFORMATION:
; APPLICANT: Kazuyoshi YAMAOKA et al.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING
; TITLE OF INVENTION: TRYPSIN-LIKE ENZYME AND PROCESS FOR PRODUCING THE ENZYME
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,448C
; FILING DATE: July 28, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
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RESULT 14
US-09-370-838-79
; Sequence 79, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 2, 2003, 02:42:05 ; Search time 391.32 Seconds
(without alignments)

3662.446 Million cell updates/sec

Title: US-09-607-745-2

Perfect score: 2342

Sequence: 1 MDPDSQPLNSLDVKPLRP.....VYTKVSAYLWIIYVWKAEL 435

Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-MAXLEN=200000000 -USER=US09607745.ecgn_1.129.eunat_01122003_160940_10006
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

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2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
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12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq:*
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15: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2338	99.8	2038	12	US-10-180-719-18

Sequence 18, Appl

2	2337	99.8	2031	9	US-09-851-588-7
3	2337	99.8	2307	14	US-10-097-340-317
4	2337	99.8	2307	14	US-10-171-311-217
5	2329	99.4	2165	12	US-10-101-510-634
6	2324	99.2	2079	9	US-09-851-588-5
7	2324	99.2	2079	11	US-09-776-191-71
8	2324	99.2	2079	14	US-10-264-820-22
9	2324	99.2	2079	14	US-10-254-289-1
10	2319	99.0	2137	11	US-09-776-131-3
11	2297.5	98.1	2063	11	US-09-888-257A-2
12	2297.5	98.1	2063	11	US-09-946-374-274
13	2297.5	98.1	2063	12	US-10-015-387A-274
14	2297.5	98.1	2063	12	US-10-063-735-111
15	2297.5	98.1	2063	12	US-10-006-130A-274
16	2297.5	98.1	2063	12	US-10-193-672-329
17	2297.5	98.1	2063	12	US-10-006-172A-274
18	2297.5	98.1	2063	12	US-10-187-749-329
19	2297.5	98.1	2063	12	US-10-194-457-329
20	2297.5	98.1	2063	12	US-10-184-642-329
21	2297.5	98.1	2063	12	US-10-196-747-329
22	2297.5	98.1	2063	12	US-10-015-322A-274
23	2297.5	98.1	2063	12	US-10-017-253A-274
24	2297.5	98.1	2063	12	US-10-173-689-329
25	2297.5	98.1	2063	12	US-10-173-690-329
26	2297.5	98.1	2063	12	US-10-173-691-329
27	2297.5	98.1	2063	12	US-10-173-692-329
28	2297.5	98.1	2063	12	US-10-173-694-329
29	2297.5	98.1	2063	12	US-10-173-698-329
30	2297.5	98.1	2063	12	US-10-173-699-329
31	2297.5	98.1	2063	12	US-10-173-707-329
32	2297.5	98.1	2063	12	US-10-174-569-329
33	2297.5	98.1	2063	12	US-10-174-583-329
34	2297.5	98.1	2063	12	US-10-174-587-329
35	2297.5	98.1	2063	12	US-10-174-589-329
36	2297.5	98.1	2063	12	US-10-174-591-329
37	2297.5	98.1	2063	12	US-10-175-736-329
38	2297.5	98.1	2063	12	US-10-175-742-329
39	2297.5	98.1	2063	12	US-10-175-744-329
40	2297.5	98.1	2063	12	US-10-175-745-329
41	2297.5	98.1	2063	12	US-10-175-748-329
42	2297.5	98.1	2063	12	US-10-175-751-329
43	2297.5	98.1	2063	12	US-10-175-754-329
44	2297.5	98.1	2063	12	US-10-176-480-329
45	2297.5	98.1	2063	12	US-10-176-489-329

ALIGNMENTS

RESULT 1

US-10-180-719-18
; Sequence 18, Application US/10180719
; Publication No. US2003016246A1

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

;; SOFTWARE: FastSeq for Windows Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/180,719

;; FILING DATE: 25-Jun-2002

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/09/008,271

;; FILING DATE: 16-Jan-1998

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Mohan-Peterson, Sheela

;; REGISTRATION NUMBER: 41,201

;; REFERENCE/DOCKET NUMBER: PP-0458 US

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-855-0555

;; TELEFAX: 650-845-4166

;; INFORMATION FOR SEQ ID NO: 18:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 2038 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; IMMEDIATE SOURCE:

;; LIBRARY: COLNOT13

;; CLONE: 1337018

;; SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-180-719-18

Alignment Scores:

Pred. No.: 6,8e-283 Length: 2038
Score: 2338.00 Matches: 434
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.83% Indels: 0
DB: 12 Gaps: 0

US-09-607-745-2 (1-435) x US-10-180-719-18 (1-2038)

QY 1 MetAspProAspSerAspGlnProLeuAsnSerLeuAspVallyProLeuArgLysPro 20
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QY 21 ArgIleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaLeuLeuSer 40
Db 260 CGTATCCCATGGAGACCTTCAGAAAGTGGGGATCCCATCATCATAGCACTACTGAGC 319
QY 41 LeuAlaSerIleIleIleValValValbeulleLysValIleLeuAspLysTyrPhe 60
Db 320 CTGCGAGATATCATATTGTGGTGTCTCATCAAGGTGATTCTGGATAAATACTACTTC 379
QY 61 LeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAsp 80
Db 380 CTCGCGGGAGCCTCTCCACTTCATCCGAGGAAGCAGCTGTGTGACGGAGCTGGAC 439
QY 81 CysProLeuGlyGluAspGluLHisCysVallySerPheProGluGlyProAlaVal 100
Db 440 TGTCCCTTGGGGAGGACGAGGACGACGTGTCTCAAGACTTCCCGAAGGACCTGCAGTG 499
QY 101 AlaValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsn 120
Db 500 GCAGTCGCGCTCTCCAAAGGACCGATCCACACTGCAGGTGTCTGGACTCGGCCACAGGGAAC 559
QY 121 TrpPheSerAlaCysPheAspAsnPhetrGluAlaLeuAlaGluThrAlaCysArgGln 140
Db 560 TGGTCTCTGCTGTTTCGACAACTTCAGAAGCTCTCGCTGAGACAGCCTGTAGGCGAG 619
QY 141 MetGlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeu 160
Db 620 ATGGGTACACAGCAAAACCCACTTTCAGAGCTGTGGAGATGGCCACAGCAGACTG 679
QY 161 AspValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyPro 180
Db 680 GATGTTGTGAAATACACAGAAAACAGCCAGGAGCTTCGATGCGGAACCTCAAGTGGGCC 739
QY 181 CysLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThr 200

Db 740 TGTCTCTCAGGCTCCCTGGTCTCCCTGCATGCTTGGCTGTGGGAGAGCCTGAGACC 799
QY 201 ProArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIle 220
Db 800 CCCGTTGTGGTGGGGAGGAGGCTCTGTGGATCTTTGGCTTTGGCAGGTGAGATC 859
QY 221 GlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThr 240
Db 860 CAGTACGACAAACAGCAGCAGTCTGTGGAGGAGGAGCATCTCTGACCCCACTGGTCTCAGC 919
QY 241 AlaAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySer 260
Db 920 GCAGCCCACTGCTTCAGGAAACATACCGATGTCTTCAACTGGAAGGTGCGGGCAGGTCA 979
QY 261 AspLysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsn 280
Db 980 GACAAACTGGGAGCTTCCCTCCCTGGCTGTGGCCCAAGATCATCATCATGATGATTCAC 1039
QY 281 ProMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPhe 300
Db 1040 CCCATGTACCCCAAGACATGACATCGCCCTCATGAAGCTGCAGTTCACCACTTC 1099
QY 301 SerGlyThrValArgProIleCysLeuProPheAspGluGluLeuThrProAlaThr 320
Db 1100 TCAGGCACAGTCAGGCCCATCTCTCTGCCCTCTTTGATGAGGAGCTCACTCCAGCCACC 1159
QY 321 ProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIle 340
Db 1160 CCACCTCGGATCATTTGGATGGGCTTTACGAACAGATGAGGGAAGATGTCTGACATA 1219
QY 341 LeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyr 360
Db 1220 CTGCTGCAGGCGTCAGTCCAGGTCAATTGACAGCACAGCGGTCAATGCAGACGATCGTAC 1279
QY 361 GlnGlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThr 380
Db 1280 CAGGGGAGAGTACCAGAGAGATGATGTGTGAGGATCCCGAAGGGGTGTGGACACC 1339
QY 381 CysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGly 400
Db 1340 TGCAGGGTGACAGTGGTGGGCCCCCTGATGTACCATCTGACCATGGCATGTGGTGGGC 1399
QY 401 IleValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysVal 420
Db 1400 ATCGTTAGCTGGGCTATGGCTCGGGGGCCCGAGCACCCAGGAGTATATACCAAGGTC 1459
QY 421 SerAlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
Db 1460 TCAGCCTATCTCACTGATCTCAATGTCTGGAAGGCTGAGCTG 1504

RESULT 2

US-09-851-588-7

; Sequence 7, Application US/09851588

; Patent No. US20020042067A1

; GENERAL INFORMATION:

; APPLICANT: Mack, David

; APPLICANT: Gish, Kurt C.

; APPLICANT: Wilson, Keith E.

; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, A

; FILE REFERENCE: A-68829-1/DUB/JUD/AMS

; CURRENT APPLICATION NUMBER: US/09/851,588

; CURRENT FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: US 09/642,252

; PRIOR FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: US 09/656,002

; PRIOR FILING DATE: 2000-09-06

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 2081

; TYPE: DNA

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 317
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2307)
; OTHER INFORMATION: n = A,T,C or G
US-10-097-340-317

Alignment Scores:

Pred. No.: 1.1e-282 Length: 2307
Score: 2337.00 Matches: 434
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 14 Gaps: 0

US-09-607-745-2 (1-435) x US-10-097-340-317 (1-2307)

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QY 22 IleProMetGluThrPheArgLysValGlyLeuProIleLeuAlaLeuLeuSerLeu 41
DB 344 ATCCCATGAGAGACCTTCAGAAAGGTGGGATGCCATCATCATAGCACTACTGAGGCTG 403

QY 42 AlaSerIleIleValValValValLeuLeuLeuValLeuAspLysTyrPheLeu 61
DB 404 GCGAGTATCATCATGTGGTGTCTCATCAAGGTGATTCGGATAAATACTACTTCTC 463

QY 62 CysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCys 81
DB 464 TCGGGGAGCCTCTCCACTTCATCCGAGGAGAGCAGCTGTGTGACGAGAGCTGGATGT 523

QY 82 ProLeuGlyGluAspGluGluHisCysVallySerPheProGluGlyProAlaValAla 101
DB 524 CCCPTGGGGAGGACGAGGACACTGTGTCAAGAGCTTCCCGAAGGCGCTGCAGTGGA 583

QY 102 ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp 121
DB 584 GTCCGCTCTCTCAAGGACCGATCCACTGCAGTGTCTGGACTCGGCCACAGGAACTGG 643

QY 122 PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMet 141
DB 644 TTCTTGCTCTTTCGACAACTTCACAGAGCTCTCGCTGAGACAGCCTGTAGGCAGATG 703

QY 142 GlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAsp 161
DB 704 GGCTACAGCAGCAAAACCCACTTTTCAGAGCTGTGGAGATTGGCCCAAGACAGGATCTGGAT 763

QY 162 ValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCys 181
DB 764 GTTTTGAATACAGAAACAGCAGAGCTTGCATCGCGAACTCAAGTGGGCGCTGT 823

QY 182 LeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPro 201
DB 824 CTCCTCAGGCTCCCTGGTCTCCCTGCACGTCTTGCTGTGGAGATTGGCCCAAGACCCCC 883

QY 202 ArgValValGlyGlyGluAlaSerValAspSerTrpProTrpGlnValSerIleGln 221
DB 884 CGTGTGGTGGGAGAGGCGCTCTGTGGATTCTTGGCCTTGGCAGTCAAGCATCCAG 943

QY 222 TyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAla 241
DB 944 TACGACAAACAGCAGCTGTGGAGGAGCATCTCGACCCCGCTTGGTCTCAGCGCA 1003

QY 242 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 261
DB 1004 GCCCACTCTTCAGGAACATACCGATGTGTTCACCTGGAGAGTGGCGGAGGCTCAGAC 1063

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QY 262 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPro 281
DB 1064 AAACCTGGGAGCTTCCCATCCCTGGCTGTGGCCAGATCATCATCTGAATCAACCCC 1123

QY 282 MetTyrProLysAspAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 301
DB 1124 ATGTACCCCAAGACAAATGACATCGCCCTCATGAAGCTGCAGTCCCACTCACTTTCTCA 1183

QY 302 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 321
DB 1184 GGCACAGTCAAGCCCATCTGTCTGCCCTCTTTGTATGAGGAGCTCACTCCAGCCACCCCA 1243

QY 322 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu 341
DB 1244 CTCTGGATCATTTGATGGGCTTTACGAAGCAGATGGAGGAGATGTCTGACATCTG 1303

QY 342 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrGln 361
DB 1304 CTCAGCGCTCAGTCCAGGTCAATTGACACACACGGTGCAATGCAGACGATGGGTACCAG 1363

QY 362 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 381
DB 1364 GCGGAGTCAACCGAAGATGATGTGTGCGGCAATCCCGAAGGGGTGGACACCTGC 1423

QY 382 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 401
DB 1424 CAGGCTGACAGTGGTGGGCGCTGTATGATCAATCTGACCAATCTGACCAAGTGTGGGATC 1483

QY 402 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 421
DB 1484 GTTAGTGGGCTGTATGGCTGCGGGGCGGAGACCCCAAGGATATACACCAAGGTCTCA 1543

QY 422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
DB 1544 GCTTACTCACTGATCTACATATGCTGGAAGGCTGAGCTG 1585

RESULT 4
US-10-171-311-217
; Sequence 217, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 1691, 1698, 1705, 1708, 1709, 1713, 1717, 1720, 1724, 1728,
; LOCATION: 1733, 1741, 1746, 1748, 1755, 1770, 1774, 1791, 1802, 1821,
; LOCATION: 1838, 1856, 1859, 1864, 1908, 1959, 1997, 2012, 2038, 2143
; OTHER INFORMATION: n = A,T,C or G

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US-10-171-311-217

Alignment Scores:

Pred. No.: 1,1e-282 Length: 2307
 Score: 2337.00 Matches: 434
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 14 Gaps: 0

US-09-607-745-2 (1-435) x US-10-171-311-217 (1-2307)

QY 2 AspProAspSerAspGlnProLeuAsnSerLeuAspVallysProLeuArgLysProArg 21
 DB 284 GATCTTCAGTGCATCACTCTGACAGCTCGATGTAACCCCTGCGCAACCCCTG 343
 QY 22 IleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaLeuLeuSerLeu 41
 DB 344 ATCCCCATGGAGACCTTCAGAAAGGTGGGATCCCCATCATCATAGCACTACTAGCCCTG 403
 QY 42 AlaSerIleIleIleValValValLeuIleLysValIleLeuAspLysTyrPheLeu 61
 DB 404 GGGAGTATCATATTGTGTGTCCTCATCAAGGTGATTCTGGATAAATACTACTTCTCTC 463
 QY 62 CysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCys 81
 DB 464 TGGGGGAGCCTCTCCACTTCATCCCGAGGAGCAGCTGTGTGACCGAGAGCTGGACTGT 523
 QY 82 ProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaValAla 101
 DB 524 CCCTTGGGGAGGAGCAGGAGCACTGTGTCAAGAGCTTCCCGAAGGGCTGCGAGTGCCA 583
 QY 102 ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp 121
 DB 584 GTCCGGCTCTCCAAAGACCGCATCCACTCGAGGTGTGACTCGGCCACAGGAACTGG 643
 QY 122 PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMet 141
 DB 644 TTCTCTGCTGTTTCACACACTTCACAGAGCTCTGCTGAGCAGCCTGTAGCGAGATG 703
 QY 142 GlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAsp 161
 DB 704 GGCTACAGCAGCAAAACCCACTTTTCAGAGCTGTGGAGATTGGCCACAGCAGGATCTGGAT 763
 QY 162 ValValGluIleThrGluAsnSerGlnGluLeuArgMetArgLysSerSerGlyProCys 181
 DB 764 GTTGTTGAAATACAGAAACACCGACGAGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGT 823
 QY 182 LeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPro 201
 DB 824 CTCTCAGGCTCCCTGCTCTCCCTGCATGTCCTGCTGTGGGAGAGCCTGAAGACCCCC 883
 QY 202 ArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGln 221
 DB 884 CGTGTGTGGTGGGAGGAGGCTCTGTGGATTCTTGGGCTTGGCAGAGTCAAGCTCCAG 943
 QY 222 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 241
 DB 944 TAGCAAAACAGCAGCGTCTGTGGAGGAGCATCTGGACCCCACTGGGTCCTCAACCGGCA 1003
 QY 242 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 261
 DB 1004 GCCCACTGCTTCAGAAACATACCGATGTGTTCACTGGAGAGTGTGGGCGAGGCTCAGAC 1063
 QY 262 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPro 281
 DB 1064 AAACCTGGCAGCTTCCCATCCCTGGCTGTGGCCAAAGATCATCATATTGAATTCACCCC 1123
 QY 282 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 301
 DB 1124 ATGTACCCCAAGACATATGATCGCCCTCATGAAGCTGCGAGTTCACACTCACTTTCTCA 1183
 QY 302 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 321

DB 1184 GGCACAGTCAGGCCCATCTGTCTGCCCTTTCTTTGATGAGGAGCTCACTCAGCCACCCCA 1243
 QY 322 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 341
 DB 1244 CTCTGGATCATTTGGATGGGCTTTTACGAAGCAGAGATGGAGGGAAGATGTCTGCATACTG 1303
 QY 342 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 361
 DB 1304 CTCGAGGCGTCAGTCCAGGTCAATGCACAGCACACCGTGCATATGCAGCAGCATCGTACCAG 1363
 QY 362 GlyGluValThrGluLysMetCysAlaGlyIleProGluGlyGlyValAspThrCys 381
 DB 1364 GGGAGAGTCACCGAGAGATGATGTGCAGGATCCCCGGAAGGGGTGTGGACACTGC 1423
 QY 382 GlnGlyAspSerGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 401
 DB 1424 CAGGCTGACAGTGTGGGCCCTGATGTACCAATCTGACCACTGGCATCTGGTGGGCATC 1483
 QY 402 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValThrLysValSer 421
 DB 1484 GTTAGCTGGGGCTATGGCTGCGGGGGCCGAGCACCCGAGGAGTATACACCAAGGTCTCA 1543
 QY 422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
 DB 1544 GCCTATCTCACTGGATCTACATGTCTGGAGAGCTGAGCTG 1585

RESULT 5

US-10-101-510-634
 ; Sequence 634, Application US/10101510
 ; Publication No. US20030148295A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WAN, JACKSON
 ; APPLICANT: WANG, YIXIN
 ; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
 ; FILE REFERENCE: 15117.0012
 ; CURRENT APPLICATION NUMBER: US/10/101,510
 ; CURRENT FILING DATE: 2002-03-20
 ; PRIOR APPLICATION NUMBER: 60/276,947
 ; PRIOR FILING DATE: 2001-03-20
 ; NUMBER OF SEQ ID NOS: 805
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 634
 ; LENGTH: 2165
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-101-510-634

Alignment Scores:

Pred. No.: 1,01e-281 Length: 2165
 Score: 2329.00 Matches: 435
 Percent Similarity: 99.77% Conservative: 0
 Best Local Similarity: 99.77% Mismatches: 0
 Query Match: 99.44% Indels: 1
 DB: 12 Gaps: 0

US-09-607-745-2 (1-435) x US-10-101-510-634 (1-2165)

QY 1 MetAspProAspSerAspGlnProLeuAsnSerLeuAspVallysProLeuArgLysPro 20
 DB 310 ATGGATCTTCAGAGTATCACTCTGAACAGCCTCGATGTCAAAACCCCTGGCAACCC 369
 QY 21 ArgIleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaLeuSer 40
 DB 370 CGTATCCCCATGGAGACCTTCAGAAAGGTGGGATCCCCATCATCATAGCACTACTGAGC 429
 QY 41 LeuAlaSerIleIleValValValLeuIleLysValIleLeuAspLysTyrPhe 60
 DB 430 CTGGCGAGTATCATATTGTGTGTCCTCATCAAGGTGATTCTGGATAAATACTACTTTC 489
 QY 61 LeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAsp 80
 DB 490 CTCTGGGGCAGCCTCTCCACTTCATCCGAGGAGCAGCTGTGTGACGGAGCTGGAC 549

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QY 81 CysProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaVal 100
Db 550 TGTCCCTTGGGGAGGACGAGGACCTGTGTCAAGAGCTTCCCGAAGGSCCTGCAGTG 609
QY 101 AlaValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsn 120
Db 610 GCAGTCGCGCTCTCAAGGACCGATCCACACTGCAGGTGTGGACTCGGCCACAGGGAAC 669
QY 121 TrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGln 140
Db 670 TGGTCTCTGCTGCTTTCGACCACTTCACAGAGCTCTCGTGTAGACAGCCCTGTAGCAG 729
QY 141 MetGlyTyrSerSerLysProThrPheArgAlaValGluLeGlyProAspGlnAspLeu 160
Db 730 ATGGGCTACAGCAGCAAAACCCACTTCAGAGCTGTGGAGATTGGCCACAGGATCTG 789
QY 161 AspValValGluLeuThrGluAsnSerGlnGlu-LeuArgMetArgAsnSerSerGlyPr 180
Db 790 GATGTTTGTGAATCACAGAAACAGCCAGGAGGCTTCGCATGGCGAACTCAAGTGGGCC 849
QY 180 oCysLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysTh 200
Db 850 CTGCTCTCAGGCTCCCTGGTCTCCCTGCATGCTCTTGCCCTGTGGAGAGCCCTGAGAC 909
QY 200 rProArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIl 220
Db 910 CCCCCTGTGTGGTGGGGAGGAGGCTCTGTGGATTCTTTGGCTTGGCAGGTACAGAT 969
QY 220 eGlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuTh 240
Db 970 CCAGTACGACAAACAGACGCTGTGGAGGAGGATCCCTGGACCCCACTCGGTCCTCAC 1029
QY 240 rAlaAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySe 260
Db 1030 GGCAGCCCACTGCTTCAGAAACATACCGATGTGTTCACTGGAGGTGGGGAGGCTC 1089
QY 260 rAspLysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAs 280
Db 1090 AGACAACTGGGCAGCTCCCATCCCTGGCTGTGGCCCAAGATCATCAITGAATTCAA 1149
QY 280 nProMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPh 300
Db 1150 CCCCATGTACCCCAAGACATGATCGCCCTCATGAAGTGCAGATTCCCACTCACTTT 1209
QY 300 eSerGlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaTh 320
Db 1210 CTCAGGCACAGTCAGGCCCATCTGTCTGCCCTCTTTGATCAGGAGCTCACTCCAGCCAC 1269
QY 320 rProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIl 340
Db 1270 CCCACTGTGATCATTTGATGGGCTTTACGAAGCAGAAATGGAGGAGATGTCTGACAT 1329
QY 340 eLeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTy 360
Db 1330 ACTGCTGCAGCGCTAGTCCAGGTCAATTGACAGACACGGTGCATGACAGCATGCGTA 1389
QY 360 rGlnGlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspTh 380
Db 1390 CCAGGGGAGNATCCCGAGAGATGATGTGTGAGGCATCCGGAAGGGGCTGTGGACAC 1449
QY 380 rCysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGl 400
Db 1450 CTGCCAGGCTGACAGTGTGGGCCCCCTGATGTACCAATCTGACCAAGTGCATGTGGTGGG 1509
QY 400 YIleValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysVa 420
Db 1510 CATGTTAGCTTGGGCTTAGCTGGGGGGCCCCAGACCCCGAGAGATACACCAAGGT 1569
QY 420 lSerAlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
Db 1570 CTCAGCCTATCTCAACTGATCTACATGTCTGGNAGGCTGAGCTG 1615
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RESULT 6

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US-09-851-588-5
; Sequence 5, Application US/09851588
; Patent No. US20020042067A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt C.
; APPLICANT: Wilson; Keith E.
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AI
; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-68829-1/DJB/JJD/AMS
; CURRENT APPLICATION NUMBER: US/09/851,588
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/642,252
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: US 09/656,002
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2079
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-851-588-5
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Alignment Scores:

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Pred. No.: 4,03e-281 Length: 2079
Score: 2324.00 Matches: 434
Percent Similarity: 99.77% Conservative: 0
Best Local Similarity: 99.77% Mismatches: 1
Query Match: 99.23% Indels: 1
DB: 9 Gaps: 0
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US-09-607-745-2 (1-435) x US-09-851-588-5 (1-2079)

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QY 2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg 21
Db 217 GATCCTGACAGTATCAACCTCTGAACAGCTCGATGTCAACCCCTGCGCAAAACCCCGT 276
QY 22 IleProMetGluThrPheArgLys-ValGlyIleProIleIleIleAlaLeuSerLe 41
Db 277 ATCCCATGAGACCTTCAGAAAGTGGGGATGCCCATCATCATAGCATCTACTAGCCT 336
QY 41 uAlaSerIleIleIleValValValLeuIleLysValIleLeuAspLysTyrTyrPheLe 61
Db 337 GCGCAGTATCATCATTTGTTGCTCATCAAGGTGATTCTGATAATAATACTACTTCT 396
QY 61 uCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCy 81
Db 397 CTGCGGCGACCTCTCCACTTCATCCGAGAGAGCAGCTGTGTACGAGAGCTGGACTG 456
QY 81 sProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaValAl 101
Db 457 TCCCTTGGGGAGGACGAGGAGGACCTGTGTCAAGAGCTTCCCGAAGGGCTGCAGTGGC 516
QY 101 aValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTr 121
Db 517 AGTCCGCTCTCCAGGACCGATCCACACTGCAGGTGTGTGACTCGGCCACAGGAACTG 576
QY 121 pPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMe 141
Db 577 GTTCTCTGCCCTGTTCGACAACTTCAGAAAGCTCTCGCTGACAGACCTGTAGGAGAT 636
QY 141 tGlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAs 161
Db 637 GGCTACAGCAGCAAAACCCACTTTTCAGAGCTGTGGAGATTGGCCACAGCATCTGGA 696
QY 161 pValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCy 181
Db 697 TGTGTTGAAATCACAGAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGCCCTG 756
QY 181 sLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPr 201
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Db 757 TCCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGGGAGAGCCTGAAGACCCC 816
QY 201 oArgValValValValValValValValValValValValValValValVal 221
Db 817 CCGTGTGGTGGTGGGAGAGGCTCTGTGGATCTTGGCCCTTGGCAGGTCAATCCA 876
QY 221 nTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAl 241
Db 877 GTACGACAAACAGCAGCTCTGTGAGGAGCACTCTGGACCCCACTGGGTCTCACGGC 936
QY 241 aAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAs 261
Db 937 AGCCCACTGCTTCAGGAAACATACCGATGTGTTCACTGGAAGTGGCGGCGAGCTCAGA 996
QY 261 pLysLeuGlySerPheProSerIleValAlaValIleIleIleIleIleIleIle 281
Db 997 CAAACTGGGAGCTTCCCATCCCTGGCTGGCGCAGATCATCATCATTAATCAACCC 1056
QY 281 oMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSe 301
Db 1057 CATGTACCCCAAGACATGACATCGCCCTCATGAGCTGCACTTCCCACTCACTTCTC 1116
QY 301 rGlyThrValArgProLysLeuProPhePheAspGluLeuThrProAlaThrPr 321
Db 1117 AGGCACAGTCAGGCCCATCTGTCTGCCCTCTTTGATGAGGAGCTCACTCCAGCCACCC 1176
QY 321 oLeuTrpIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 341
Db 1177 ACTCTGATCATGTGATGGGCTTTACAGACAGATGGAGGAGATGCTGCATCACT 1236
QY 341 uLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaTyrGl 361
Db 1237 GCTGCAGCGCTCAGTCCAGCTCATTGACAGCACACGCTGCAATGACAGCTGACCA 1296
QY 361 nGlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyValAspThrCy 381
Db 1297 GGGGGAAGTACCAGAGAGATGATGTGTGAGGATCCCGAGGAGCTGTCAGCACCTG 1356
QY 381 sGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGly 401
Db 1357 CAGGGTGCAGTGTGGGCCCCGTGATGATACCAATCTGACAGTGGCATGTGGGGCAT 1416
QY 401 eValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValse 421
Db 1417 CGTTAGTGGGCTATGCTGCGGGGCCCGAGACCCAGAGTATACACCAAGTCTC 1476
QY 421 rAlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
Db 1477 AGCCTATCTCAACTGGATCTACAATGTCTGGAGGCTGAGCTG 1519

RESULT 7
US-09-776-191-71
; Sequence 71, Application US/09776191
; Publication No. US2003019168A1
; GENERAL INFORMATION:
; APPLICANT: Edwin L. Madison
; APPLICANT: Edgar O. Ong
; APPLICANT: Jiunn-Chern Yeh
; APPLICANT: Corvas International, Inc.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: TRANSMEMBRANE SERINE PROTEASES, THE ENCODED PROTEINS AND
; TITLE OF INVENTION: METHODS BASED THEREON
; FILE REFERENCE: 24745-1607
; CURRENT APPLICATION NUMBER: US/09/776,191
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,124
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/234,840
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/179,982
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 60/183,542
; PRIOR FILING DATE: 2000-02-18
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; PRIOR APPLICATION NUMBER: 09/657,968
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 2079
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (251) ... (1522)
; OTHER INFORMATION: Nucleotide sequence encoding transmembrane
; OTHER INFORMATION: protease, serine 4 (TMPRSS4)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM016425
; DATABASE ENTRY DATE: 2000-11-06
US-09-776-191-71

Alignment Scores:
Pred. No.: 4,03e-281 Length: 2079
Score: 2324.00 Matches: 434
Percent Similarity: 99.77% Conservative: 0
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.23% Indels: 1
DB: 11 Gaps: 0

US-09-607-745-2 (1-435) x US-09-776-191-71 (1-2079)
QY 2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg 21
Db 217 GATCTCTGACAGTATCAACCTCTGAACAGCTCGATGTCAACCCCTGCGCAACCCCGT 276
QY 22 IleProMetGluThrPheArgLys-ValGlyIleProIleIleIleAlaLeuSerLe 41
Db 277 ATCCCCATGAGACCTTCAGAAAGTGTGGGATCCCATCATCATGACACTACTGAGCCT 336
QY 41 uAlaSerIleIleIleValValValLeuIleLysValIleLeuAspLysTrpTyrPheLe 61
Db 337 GCGGAGTATCATTTGTGGTGTCTCTCATCAGGTGATTCGGATAAATACTACTTCTCT 396
QY 61 uCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCy 81
Db 397 CTCGGGCGACCTCTCCACTTCATCCGAGGAAGCAGCTGTGTGACGAGCTGGAGCTG 456
QY 81 sProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaValAl 101
Db 457 TCCCTTTGGGGGAGGAGGAGGAGCAGCTGTGTCAAGAGCTTCCCGGAGGGGCTGCGAGTGGC 516
QY 101 aValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTr 121
Db 517 AGTCCGCTCTCCAAAGGACCGATCCACATGCGAGGTGTGGACTCGGCCACAGGGAATCG 576
QY 121 pPheSerAlaCysPheAspAsnPhetrGluAlaLeuAlaGluThrAlaCysArgGlnMe 141
Db 577 GTTCTCTGCTGCTTTTCGACAACTTCACAGAGCTCTCGCTGACAGACCTGTAGGCAGAT 636
QY 141 tGlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAs 161
Db 637 GGGCTACAGCAGCAAAACCCACTTTCAGAGCTGTGGAGATTGGCCCAACAGAGATCTGGA 696
QY 161 pValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCy 181
Db 697 TGTGTGTGAATCACAAGAAACAGCCAGGAGCTTCGATGCCGAATCTCAAGTGGGCGCTG 756
QY 181 sLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPr 201
Db 757 TCTCTCAGGCTCCCTGCTCTCCCTGCACTGTCTTGCCTGTGGGAGAGCCTGAAGACCCC 816
QY 201 oArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGl 221
Db 817 CCGTGTGGTGGTGGGAGGAGGAGGCTCTGTGGATTCTTGGCTTGGCAGTCAAGTCAATCCA 876
QY 221 nTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAl 241
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Db 877 GTACGACAAACAGCAGCTCTGGAGGAGCATCTCGACCCCACTGGCTCCTCACGGC 936
Qy 241 aAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAs 261
Db 937 AGCCCACTGCTTCAGAAACATACCGATGTTCACCTGGGAAGGTCCGGCAGGCTCAGA 996
Qy 261 pLysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPr 281
Db 997 CAAACTGGGAGCTTCCCATCCCTGGCTGTGGCCCAAGATCATCATTAATGAATCAACCC 1056
Qy 281 oMetTrpProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSe 301
Db 1087 CATGTACCCCAAGAACATGACATGCCCTCATGAAGCTGCAGTTCCTCCCACTCATTCTC 1116
Qy 301 rGlyThrValArgProLysCysLeuProPhePheAspGluGluLeuThrProAlaThrPr 321
Db 1117 AGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTGTATGAGGAGCTCATCTCCAGCCACCC 1176
Qy 321 oLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLe 341
Db 1177 ACTCTGGATCATTTGATGGGCTTTACGAAGCAGAATGCGAGGAAGATGTCTGCATACT 1236
Qy 341 uLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrl 361
Db 1237 GCTCAGCGCTCAGTCCAGGTCATTCACAGCACACCGGTGCATGCAGACGATGCGTACCA 1296
Qy 361 nGlyLeuValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCy 381
Db 1297 GGGGAAGTCACCGAAGATGATGTGCGAGGCATCCCGNAGGGGTGGACACCTG 1356
Qy 381 sGlnGlyAspSerGlyProLeuMetTrpGlnSerAspGlnTrpHisValValGlyI 401
Db 1357 CCAGGTCACAGTGTGGGCCCTCATGTATGACCACTGACCACTGGCATGTGTGGCAT 1416
Qy 401 eValSerTrpGlyTrpGlyCysGlyGlyProSerThrProGlyValThrLysValSe 421
Db 1417 GCTTAGCTGGGCTATGGCTGGGGGGCCGAGCACCCGAGGATATACCAAGGTCTC 1476
Qy 421 rAlaTrpLeuAsnTrpIleTrpAsnValTrpLysAlaGluLeu 435
Db 1477 AGCCTATCTCACTGATCTACATGTCTGGGAAGGCTGAGCTG 1519
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RESULT 8

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US-10-264-820-22
; Sequence 22, Application US/10264820
; Publication No. US20030108926A1
; GENERAL INFORMATION:
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030108926A1el Methods of Diagnosing Colorectal Cancer,
; Publication No. US20030108926A1
; TITLE OF INVENTION: Compositions, and Methods of Screening for Colorectal
; TITLE OF INVENTION: Cancer Modulators
; FILE REFERENCE: 018501-006141US
; CURRENT APPLICATION NUMBER: US/10/264,820
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/268,866
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: US 09/435,945
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/436,983
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/450,857
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: US 09/453,850
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 09/493,444
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 09/525,993
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2079
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CJA8 cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (251)..(1522)
; OTHER INFORMATION: human CGA8
US-10-264-820-22

Alignment Scores:
Pzed. No.: 4,03e-281 Length: 2079
Score: 2324.00 Matches: 434
Percent Similarity: 99.77% Conservative: 0
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.23% Indels: 1
DB: 14 Gaps: 0
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US-09-607-745-2 (1-435) x US-10-264-820-22 (1-2079)

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Qy 2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg 21
Db 217 GATCCTGACAGTGATCAACCTCTGAACAGCTCGATGTCAACCCCTGGCAACCCGCT 276
Qy 22 IleProMetGluThrPheArgLys-ValGlyIleProIleIleIleAlaLeuSerLe 41
Db 277 ATCCCCATGGAGACCTTCAGAAAGTGTGGGATCCCATCATCATAGCACTACTGAGCCT 336
Qy 41 uAlaSerIleIleIleValValValLeuIleLysValIleLeuAspLysTrpTrpPheLe 61
Db 337 GCCGAGTATCATCATTTGTGTGTTCCTCATCAAGGTGATTCGTGATAAATACTACTTCT 396
Qy 61 uCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCy 81
Db 397 CTGGCGGACGCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTACGAGAGCTGGAGTG 456
Qy 81 sProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaValAl 101
Db 457 TCCCTTGGGGGAGGACGAGGAGCAGCTGTGTCAAGAGCTTCCCGAAGGCGCTGCAGTGGC 516
Qy 101 aValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTr 121
Db 517 AGTCGGCTCTCCAAAGACCGATCCACACTGCAGGTGTGAGATTCGGCCACAGGAACTG 576
Qy 121 pPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMe 141
Db 577 GTTCTCTGCTGTTCGACAACTTCACAGAAGCTCTCGCTCAGACAGGCTGTAGGCAGAT 636
Qy 141 tGlyTrpSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAs 161
Db 637 GGGCTACAGCAGCAAAACCCACTTTTCAGAGCTGTGAGATTTGGCCACAGACGATCTGGA 696
Qy 161 pValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCy 181
Db 697 TGTGTGAAATCAGAAAAACAGCCAGGAGCTTCGCATGCGGAACCTCAGTGGGCCCTG 756
Qy 181 sLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPr 201
Db 757 TCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGGCTGTGGGAAGAGCCTGAAGACCC 816
Qy 201 oArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGl 221
Db 817 CCGTGTGTGGTGGGAGGAGGCGCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCA 876
Qy 221 nTrpAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAl 241
Db 877 GTACGACAAACAGCACGCTCTGTGGAGGAGGATCTCTGAGACCCCACTGGGCTCCACGCG 936
Qy 241 aAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAs 261
Db 937 AGCCCACTGCTTCAGGAACATACCGATGTGTCACTGGAGGTGGGGAGGCTCAGA 996
Qy 261 pLysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPr 281
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Db 997 CAACCTGGGAGCTTCCATCCCTGGCTGGCCAGATCATCATGATTCATCC 1056
Qy 281 oMetTyPrDlysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSe 301
Db 1057 CATGTACCCCAAGACAAATGATGAGCCCTCATGAGCTGAGTCCCATCTCTC 1116
Qy 301 rGlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPr 321
Db 1117 AGGCACAGTCCAGGCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCATCCAGCCACCC 1176
Qy 321 oLeuTriPilleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLe 341
Db 1177 ACTCTGATCATTTGATGGGCTTTTCAAGACAGAAATGGAGGAGATGCTGACATCT 1236
Qy 341 uLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaThrGly 361
Db 1237 GCTGCAGGCTCAGTCCAGGTCATTGACAGCACAGGTCGAATGCAGACGATGGGTACCA 1296
Qy 361 nGlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCy 381
Db 1297 GGGGGAAGTCCACGAGAGATGATGTGCGAGGATCCCGGAAGGGGTGAGACCTG 1356
Qy 381 sGlnGlyAspSerGlyGlyProLeuMetTyPrGlnSerAspGlnTrpHisValValGlyI 401
Db 1357 CCAGGTTGACAGTGGTGGGCCCTTGATGTACCATCTGACAGTGGCATGTGGTGGCAT 1416
Qy 401 eValSerTrpGlyTyrglyCysGlyGlyProSerThrProGlyValTyThrLysValSe 421
Db 1417 CGTTAGTGGGCTATGCTGCGGGGCCCGAGCAGCCCGAGGATATACACCAAGGTCTC 1476
Qy 421 rAlaTyLeuAsnTrpIleTyrsenValTrpLysAlaGluLeu 435
Db 1477 AGCCTATCTCACTGATCTACATGCTTGAAGGCTGAGCTG 1519
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RESULT 9

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US-10-254-289-1
; Sequence 1, Application US/10254289
; Publication No. US20030118509A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
; OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-69108/DUB/JDD/AMS
; CURRENT APPLICATION NUMBER: US/10/254,289
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US/09/656,002
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/525,993
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 09/493,444
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US 00/07044
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2079
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-254-289-1

Alignment Scores:
Pred. No.: 4,03e-281 Length: 2079
Score: 2324.00 Matches: 434
Percent Similarity: 99.77% Conservative: 0
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.23% Indels: 1
DB: 14 Gaps: 0

US-09-607-745-2 (1-435) x US-10-254-289-1 (1-2079)
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Qy 2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg 21
Db 217 GATCCTGACAGTATCAACCTCTGAACAGCCTCGATGTCAACCCCTGCGCAAAACCCCGT 276
Qy 22 IleProMetGluThrPheArgLys-ValGlyIleProIleIleIleAlaLeuLeuSerLe 41
Db 277 ATCCCATGAGACCTTCAGAAAGTGTGGGATCCCATCATCATGACCATCTAGACCT 336
Qy 41 uAlaSerIleIleIleValValLeuIleLysValIleLeuAspLysTrpTyrrPheLe 61
Db 337 GCGGAGTATCATATTGTGTCTCTCATCAAGGTGATTCTGGATAAAATACTACTTCT 396
Qy 61 uCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyIleLeuAspCy 81
Db 397 CTCGCGGACCTCTCCACTTCATCCGAGGAAGCAGCTGTGTGACGAGAGCTGGAGCTG 456
Qy 81 sProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaValAl 101
Db 457 TCCTTTGGGGAGGACGAGGAGCCTGTGTCAAGAGCTTCCCGAGGGGCTGCAGTGGC 516
Qy 101 aValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTr 121
Db 517 AGTCCGCTCTCCAGACCGATCCACACTGCAAGTGTGCACTCGGCCACACAGGAACTG 576
Qy 121 pPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMe 141
Db 577 GTTCTCTGCTGTTCGACAACTTCAGAAAGCTCTGCTGAGACAGCCTGTGAGGAGAT 636
Qy 141 tGlyTyrrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAs 161
Db 637 GGCTACAGCAGCAAAACCCACTTTTCAGAGCTGTGGAGATTGGCCACAGCAGGATCTGGA 696
Qy 161 pValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCy 181
Db 697 TGTGTGTGAATCACAGAAAAACAGCAGGAGCTTCGCATCGGAACCTCAAGTGGGCTG 756
Qy 181 sLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuThrPr 201
Db 757 TCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGGCTGTGGGAAGAGCCTGAAGACCC 816
Qy 201 oArgValValGlyGlyGluGluAlaSerValAspSerTrpTrpGlnValSerIleG 221
Db 817 CCGTGTGGTGGTGGGAGAGAGCCCTCTGTGGATTCTTGGCCCTTGGCAGGTGACATCCA 876
Qy 221 nTyrrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAl 241
Db 877 GTACGACAAACAGCAGCTCTGTGGAGGAGCATCTTGGACCCCTGCTGGTCTCTCACGGC 936
Qy 241 aAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAs 261
Db 937 AGCCCACTGTCTCAGGAACATACCCATGTGTCACTGGAAGGTGCGGGAGGCTCAGA 996
Qy 261 pLysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPr 281
Db 997 CAACCTGGGAGCTTCCCATCCCTGGCTGTGGCCAGATCATCATCATGATTCATCAACC 1056
Qy 281 oMetTyrrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSe 301
Db 1057 CATGTACCCCAAGACAAATGACATCGCCCTCATGAAGCTCGATTCCTCACTTCTC 1116
Qy 301 rGlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPr 321
Db 1117 AGGCACAGTCCAGGCCATCTGTCTGCCCTTCTTTGATGAGGAGCTACTCCAGCCACCC 1176
Qy 321 oLeuTriPilleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLe 341
Db 1177 ACTCTGATCATTTGATGGGCTTTTCAAGACAGAAATGGAGGAGATGCTGACATCT 1236
Qy 341 uLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaThrGly 361
Db 1237 GCTGCAGGCTCAGTCCAGGTCATTGACAGCACAGGTCGAATGCAGACGATGGGTACCA 1296
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Qy 361 nGlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyValAspThrCy 381
Db 1297 GGGGAAGTCAACGAGAGATGATGTGCGAGGATCCCGAAGGGGTGTGGACACTG 1356
Qy 381 sGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValGlyIle 401
Db 1357 CCAGGTGACAGTGTGGGGCCCTGATGTACAACTCTACCAAGTGGCATGTGGGGCAT 1416
Qy 401 eValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSe 421
Db 1417 CGTAGCTGGGCTATGCTGCGGGGGCCGAGACCCAGAGATATACACCAAGGTCTC 1476
Qy 421 rAlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
Db 1477 AGCCTATCTCAACTGGATCAATGTCTGGAAGGCTGAGCTG 1519

RESULT 10
US-09-776-191-3
; Sequence 3, Application US/09776191
; Publication No. US20030119168A1
; GENERAL INFORMATION:
; APPLICANT: Edwin L. Madison
; APPLICANT: Edgar O. Ong
; APPLICANT: Jium-Chern Yeh
; TITLE OF INVENTION: CORVAS INTERNATIONAL, INC.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: TRANSMEMBRANE SERINE PROTEASES, THE ENCODED PROTEINS AND
; TITLE OF INVENTION: METHODS BASED THEREON
; FILE REFERENCE: 24745-1607
; CURRENT APPLICATION NUMBER: US/09/776,191
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,124
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/234,840
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/179,982
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 60/183,542
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: 09/657,968
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2137
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (261)...(1574)
; OTHER INFORMATION: DNA sequence encoding a transmembrane serine
; OTHER INFORMATION: protease (MTSP3) protein
US-09-776-191-3

Alignment Scores:
Pred. No.: 1 79e-280 Length: 2137
Score: 2319.00 Matches: 432
Percent Similarity: 99.54% Conservative: 0
Best Local Similarity: 99.54% Mismatches: 2
Query Match: 99.02% Indels: 0
DB: 11 Gaps: 0

US-09-607-745-2 (1-435) x US-09-776-191-3 (1-2137)

Qy 2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg 21
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Qy 22 IleProMetGluThrPheArgLysValGlyIleProIleIleAlaLeuLeuSerLeu 41
Db 330 ATCCCATGGAGACCTTCAGAAAGTGGGATCCCATCATCATAGCACTACTGAGCCTG 389
Qy 42 AlaSerIleIleIleValValValLeuIleLysValIleLeuAspLysTyrTyrPheLeu 61
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Db 390 GCGAGTATCATCTATTGTGTGTCTCTCATCAAGGTGATCTGGATAAATACTACTTCTC 449
Qy 62 CysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCys 81
Db 450 TCGGGGAGGCTCTCCACTTCATCCCGAGGAACAGCTGTGTGACGAGAGCTGGATGT 509
Qy 82 ProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaValAla 101
Db 510 CCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCGAAGGGCTCGAGTGGCA 569
Qy 102 ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp 121
Db 570 GTCCGCTCTCCCAAGGACCGATCCACTGCAGTGTCTGACTCGGCTCGGCAACAGGA 629
Qy 122 PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGluMet 141
Db 630 TTCTCTGCTGCTGTTCGACAACTTCACAGAAGCTCTCGCTGAGACAGCTGTAGGCA 689
Qy 142 GlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAsp 161
Db 690 GGCTACAGCAGCAAAACCCACTTCAGAGCTGTGGAGATTGCCCCAGACACGAGTCTG 749
Qy 162 ValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCys 181
Db 750 GTTGTGAAATCACAGAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGCCCT 809
Qy 182 LeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPro 201
Db 810 CTCTCAGGCTCCCTGGTCTCCCTGCACTGCTTGCCTGTGGAGAGCCCTGAAGACCCC 869
Qy 202 ArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGln 221
Db 870 CGTGTGTGGTGGGAGGAGGCTCTGTGGAATCTTGGCCTTGGCAGGTCAGCATCCAG 929
Qy 222 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 241
Db 930 TAGGACATACAGCAGCTCTGTGGAGGAGCATCTCGACCCCACTGGCTCTCACGCA 989
Qy 242 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 261
Db 990 GCCACCTGCTTCAGAAACATACCGATGTGTTCACTGGAAGGTGCGGGCAGGCTCAG 1049
Qy 262 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 281
Db 1050 AAATGGGAGCTTCCATCCCTGGCTGTGGCCAAAGATCATCATTAATCAACCCC 1109
Qy 282 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 301
Db 1110 ATGTACCCCAAGACAAATGACATCGCCCTCATGAAGCTGAGTTCACACTCACTTTCT 1169
Qy 302 GlyThrValArgProIleCysLeuProPheAspGluGluLeuThrProAlaThrPro 321
Db 1170 GGCACAGTCAGGCTCATCTGTCTGCCCTTTTGTAGAGAGGCTCACTCCAGCCACCCA 1229
Qy 322 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 341
Db 1230 CTCTGGATCATTTGGATGGGCTTTACGAGCAGATGGAGGAAGATGTCTGACATCTG 1289
Qy 342 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 361
Db 1290 CTGAGGCGTCACTCCAGGTCATTGACAGCACAGGTGCAATGCAGACGATGGGTAC 1349
Qy 362 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 381
Db 1350 GGGGAAGTCAACGAGAGATGATGTGCGAGGATCCCGAAGGGGTGTGGACACCTGC 1409
Qy 382 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValGlyIle 401
Db 1410 CAGGGTGACAGTGGTGGGCCCTGATGTACCAATCTGACCAAGTGGCATGTGTGGGGCAT 1469
Qy 402 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 421
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QY 382 GlnGlyAspSerGlyClyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 401
DB 1344 CAGGGTGACAGAGTGGGGCCCTGATGTACCAATCTGACAGTGGCATGTGGTGGGCATC 1403
QY 402 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrIysValSer 421
DB 1404 GTTACTGGGGTATGGCTGGGGGGCCGACGACCCAGGAGTATACACCAAGGTCTCA 1463
QY 422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
DB 1464 GCGTATCTCACTGGATCTACAAATGCTGGAAGGCTGACGCTG 1505
RESULT 12
US-09-946-374-274
; Sequence 274, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
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; PRIOR APPLICATION NUMBER: 60/098598
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/ PRIOR APPLICATION NUMBER: 60/102687
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/ PRIOR FILING DATE: 1998-10-14
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/ PRIOR APPLICATION NUMBER: 60/105002
/ PRIOR FILING DATE: 1998-10-20
/ PRIOR APPLICATION NUMBER: 60/105104
/ PRIOR FILING DATE: 1998-10-21
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/ PRIOR FILING DATE: 1998-10-22
/ PRIOR APPLICATION NUMBER: 60/105266
/ PRIOR FILING DATE: 1998-10-22
/ PRIOR APPLICATION NUMBER: 60/105693
/ PRIOR FILING DATE: 1998-10-26
/ PRIOR APPLICATION NUMBER: 60/105694
/ PRIOR FILING DATE: 1998-10-26
/ PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores:
Pred. No.: 8,51e-278
Score: 2297.50
Percent Similarity: 98.85%
Length: 2063
Matches: 429
Conservative: 0

Best Local Similarity: 98.85% Mismatches: 0
Query Match: 98.10% Indels: 5
DB: 11 Gaps: 1
US-09-607-745-2 (1-435) x US-09-946-374-274 (1-2063)
QY 2 AspProAspSerAspGlnProLeuAenSerLeuAspVallysProLeuArgLysProArg 21
DB 219 GATCCTGCACAGTATCAACCTCTGAACAGCTCGATGTCAACCCCTGCGCAACCCCGT 278
QY 22 IleProMetGluThrPheArgLysValGlyIleProIleIleLeuLeuSerLeu 41
DB 279 ATCCCATGGAGACCTTCAGAAAGGTGGGATCCCATCATCATAGACACTACTGAGCGTG 338
QY 42 AlaSerIleIleIleValValValLeuIleValIleValIleLeuAspLysTyrPheLeu 61
DB 339 GCGAGTATCATCATTTGTGTCTCATCAGGTGATTCTGGATAAATACTACTTCTCTC 398
QY 62 CysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCys 81
DB 399 TCGGGGAGCCCTCTCCACTTCATCCGAGGAACAGCTGTGTGACGAGAGCTGGACTGT 458
QY 82 ProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaValAla 101
DB 459 CCCTTGGGGAGGACGAGGAGGACTGTGTCAAGACTTCCCGAAGGGCTTCAGTGGCA 518
QY 102 ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp 121
DB 519 GTCCGGCTCTCCAAAGGACCGATCCACTGCAGCTGTGTGACTCGGCCACAGGGAACCTGG 578
QY 122 PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMet 141
DB 579 TTCTCTGCCCTGTTTCAGAACATTCACAGAGCTCTCCTGAGACAGCCTGTAGCAGATG 638
QY 142 GlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAsp 161
DB 639 GGCTACAGC-----AGAGCTGTGGAGATTGGCCCGACAGGATCTGGAT 683
QY 162 ValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCys 181
DB 684 GTTGTGTAATCAAGAAACAGCCAGAGCTTCGCATCGCGAACTCAAGTGGGCGCCCTGT 743
QY 182 LeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPro 201
DB 744 CTCTCAGGCTCCCTGTCTCCCTGCACTGTCTGTGGGAGAGCCCTGAAGACCCCC 803
QY 202 ArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGln 221
DB 804 CGTGTGGTGGGTGGGAGGAGGCTCTGTGGATTCTTGGCTTGGCAGGTTCAGCATCCAG 863
QY 222 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 241
DB 864 TACGACAAAACAGCACGCTCTGTGGAGGAGCATCTCGACCCCACTGGGTCTCAGCGCA 923
QY 242 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 261
DB 924 GCCACTGTCTCAGGAAACATACCGATGTCTCACTGGAGGTGGGGAGGCTCAGAC 983
QY 262 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleLeuGluPheAsnPro 281
DB 984 AAATGGGAGCTTCCCATCCCTGGCTGTGGCCCAAGATCATCATCATGATTAATCAACCCC 1043
QY 282 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 301
DB 1044 ATGTACCCCAAGACAAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTTCTCTCA 1103
QY 302 GlyThrValArgProIleCysLeuProPheAspGluGluLeuThrProAlaThrPro 321
DB 1104 GGCACAGTCAGGCCCATCTGTCTGCCCCCTTTTGTATGAGAGGCTCACTCAGACCAACCCA 1163
QY 322 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 341
DB 1164 CTCTGGATCATTTGGATGGGGCTTTTACAGACAGATGGAGGAGATGTCTGACATCTG 1223

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Qy 342 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAlaThrGln 361
Db 1224 CTGCAGGGCGTCAGTCCAGGTCATTGACAGCACAGCGTGCAATGCGAGACGATGGTACCAG 1283
Qy 362 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 381
Db 1284 GGGGAAGTGACCGAGAAAGATGATGTGTGACGCAATCCCGGAAGGGGGTGTGGACACCTGC 1343
Qy 382 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 401
Db 1344 CAGGGTGACAGTGTGGGCCCTGATGATGACCAATCTGACAGTGCGATGTGGTGGGCATC 1403
Qy 402 ValSerThrGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 421
Db 1404 GTTAGCTGGGCTATGGCTGGGGGGCCGAGCACCAGGAGTATACACCAAGGTCTCA 1463
Qy 422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
Db 1464 GCCTATCTCAACTGGATCTACAATGCTCGGAAGGCTGAGCTG 1505

RESULT 13
US-10-015-387A-274
; Sequence 274, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 274
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-387A-274

Alignment Scores:
Pred. No.: 8,51e-278 Length: 2063
Score: 2297.50 Matches: 429
Percent Similarity: 98.85% Conservative: 0
Best Local Similarity: 98.85% Mismatches: 5
Query Match: 98.10% Indels: 0
DB: 12 Gaps: 1

US-09-607-745-2 (1-435) x US-10-015-387A-274 (1-2063)
Qy 2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg 21
Db 219 GATCTGACAGTGATCAACCTCTGACAGCCTCGATGTCACACCCCTCGGCAACCCCGT 278
Qy 22 IleProMetGluThrPheArgLysValGlyIleProIleIleAlaLeuLeuSerLeu 41
Db 279 ATCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTAGGCCTG 338
Qy 42 AlaSerIleIleValValValLeuIleLysValIleLeuAspLysTyrThrPheLeu 61

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Db 339 GCGAGTATCATCATTTGTGGTGTCTCTCATCAAGGTGATTCTGGATAAATACTACTTCTC 398
Qy 62 CysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGlyLeuAspCys 81
Db 399 TGGGGGAGAGCTCTCCACTTCATCCCGAGGAAGAGCTGTGTGACGAGAGCTGGATGT 458
Qy 82 ProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaValAla 101
Db 459 CCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCTCGAGTGGA 518
Qy 102 ValArgLeuSerLysAspArgSerThrIleGlnValLeuAspSerAlaThrGlyAsnTrp 121
Db 519 GTCCGCTCTCCAAAGGACCATCCACTCGAGTGTGTGACTCGGCCACAGGGAACCTGG 578
Qy 122 PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMet 141
Db 579 TTCTCTGCTGTTTCGACAACTTCACAGAAGCTCTCGCTGAGACAGCTGTAGGCAGATG 638
Qy 142 GlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAsp 161
Db 639 GGCTACAGC-----AGAGCTGTGAGATTGGCCCGACAGGATCTGGAT 683
Qy 162 ValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCys 181
Db 684 GTTGTGAAATCACAGAAACAGCCAGAGCTTGCATGCGGAACCTCAAGTGGGCCCTGT 743
Qy 182 LeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPro 201
Db 744 CTCTCAGGCTCCCTGGTCTCCCTGCAGCTGTTCCTGTGGAGAGAGCTCGAAGACCCCC 803
Qy 202 ArgValValGlyGlyGluGluAlaSerValAspSerTrpProThrGlnValSerIleGln 221
Db 804 CGTGTGGTGGGTGGGGAGGAGGCTCTGTGGATTCTTGGCTTGGCAGGTGAGCATCCAG 863
Qy 222 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisIleTrpValLeuThrAla 241
Db 864 TAGACAAACAGCACAGCTCTGTGGAGGAGCATCTCGACCCCTCGGCTCTCGGCTCA 923
Qy 242 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValAlaGlySerAsp 261
Db 924 GCCCACTGCTTCAGAAACATACCGATGTGTTCACCTGGAGGTGCGGGCAGGCTCAGAC 983
Qy 262 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 281
Db 984 AAACCTGGCAGCTTCCCATCCCTGGCTGTGCCAAGATCATCATCATTAATTCAACCCC 1043
Qy 282 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 301
Db 1044 ATGTACCCCAAGACAATGACATCGCCCTCATGAAGCTGCAAGTTCACACTCACCTTCTCA 1103
Qy 302 GlyThrValArgProIleCysLeuProPheAspGluGluLeuThrProAlaThrPro 321
Db 1104 GGCACAGTCAGGCCCATCTGTCTGCCCTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1163
Qy 322 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 341
Db 1164 CTCTGGATCATTTGATGGGGCTTTTACGAAGCAGAATGAGGGAAGATGTCTGACATATG 1223
Qy 342 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 361
Db 1224 CTGAGGGCTGAGTCCAGGTCATTGACAGCACACGGTGGCAATGACAGGATGGGTACCAG 1283
Qy 362 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 381
Db 1284 GGGGAAGTCCCGAGAGATGATGTGTGAGGCAATCCCGGAAGGGGTGTGGACACCTGC 1343
Qy 382 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 401
Db 1344 CAGGGTGACAGTGTGGGCCCTCATGTACCAATCTCAGGAGTGGCATGTGTGGGCATC 1403
Qy 402 ValSerThrGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 421
Db 1404 GTTAGCTGGGCTATGGCTGGGGGGCCCGAGCACCAGGAGTATACACCAAGGTCTCA 1463

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QY 422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
Db 1464 GCCTATCTCAACTGGATCTACATGTCTGGAGGCTGAGCTG 1505

RESULT 14

US-10-063-735-111
; Sequence 111, Application US/10063735
; Publication No. US2003013882A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P323ORIC1
; CURRENT APPLICATION NUMBER: US/10/063,735
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 111
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-735-111

Alignment Scores:

Pred. No.: 8,51e-278 Length: 2063
Score: 2297.50 Matches: 429
Percent Similarity: 98.85% Conservative: 0
Best Local Similarity: 98.85% Mismatches: 0
Query Match: 98.10% Indels: 5
DB: 12 Gaps: 1

US-09-607-745-2 (1-435) x US-10-063-735-111 (1-2063)

QY 2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg 21
Db 219 GATCCTGACAGTGATCAACCTCTGACAGCCTCGATGTCAACCCCTGGCGAACCCTCGT 278
QY 22 IleProMetGluThrPheArgLysValGlyLeuProIleIleLeuLeuLeuSerLeu 41
Db 279 ATCCCATGGAGACCTTCAGAAAGGTGGGATCCCATCATCATCATGACTACTGAGCCTG 338
QY 42 AlaSerIleIleLeuValValLeuIleLysValIleLeuAspLysTyrTyrPheLeu 61
Db 339 GCAGATATCATCATGTGGTGTCTCATCAAGTGATCTGGATAAATACTACTTCCCTC 398
QY 62 CysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCys 81
Db 399 TGGCGGCAGCCTCTCCACTTCATCCCGAGGAGCAGCTGTGTGACGAGAGCTGGACTGT 458
QY 82 ProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaValAla 101
Db 459 CCCTTGGGGAGGACGAGGAGCAGTGTGTCAAGAGCTTCCCGAAGGGCCTGAGTGCGCA 518
QY 102 ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp 121
Db 519 GTCCGCTCTCCAGAGACCGATCCACTGAGCTGTGTGACTGGCCACAGGGAACCTGG 578
QY 122 PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMet 141
Db 579 TTCTCTGCTGTTCGACAACTTCACAGAGCTCTCGCTGAGCAGCTGTGAGCAGATG 638
QY 142 GlyTyrSerSerLysProThrPheArgAlaValGluLeuGlyProAspGlnAspLeuAsp 161
Db 639 GGCTACAGC-----AGAGCTGTGAGATTGGCCCGACAGCAGGATCTGGAT 683

QY 162 valvalglullethrghlunserglnghleuargmetargasnserserglyprocys 181
Db 684 GTTGTTCGAATCACAGAAACAGCCAGAGCTTCGGATCGGAACTCAGTGGGCCCCGTGT 743
QY 182 LeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPro 201
Db 744 CTCTCAGGCTCCCTGTCTCCCTGCTGCTGTTCCTGTGGAGAGAGCCCTGGAAGACCCCC 803
QY 202 ArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGln 221
Db 804 CGTGTGTGGTGGGAGGAGGAGGCTCTGTGGATTCTTGGCTTGGCAGGTGAGCATCCAG 863
QY 222 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 241
Db 864 TAGCACAAAAGCAGCAGCTCTGTGGAGGAGCATCTGGACCCCACTGGGTCTCTCAGGCA 923
QY 242 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 261
Db 924 GCCCATGTTCAGGAAACATACCGATGTTCATCTGGAAGGTGGGGCAGGCTCAGAC 983
QY 262 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleLeuGluPheAsnPro 281
Db 984 AAACCTGGCAGCTTCCCATCCCTGGCTGTGGCCAGATCATCATCATGATTGAATTCACCCC 1043
QY 282 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 301
Db 1044 ATGTACCCCAAGACAAATGACATCGCCCTCATGAAGCTGCAGTTCGCACTTCTCTCA 1103
QY 302 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 321
Db 1104 GGCACAGTCAGGCCCATCTGTCTGCCCTCTTTTGATGAGGAGCTCACTCCAGCCACCCCA 1163
QY 322 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyLysMetSerAspIleLeu 341
Db 1164 CTCTGATCATTTGATGGGCTTTACGAAGCAGATGGAGGAGATGTCTGACATACCTG 1223
QY 342 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 361
Db 1224 CTGCAGGCTCAGTCCAGGTCAATGTACACACACGCTGCAATGCACAGCATGCTGATCC 1283
QY 362 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 381
Db 1284 GGGGAAGTCACGAGAGATGATGTGTGACAGCATCCCGAAGGGGTGTGGACACCTGC 1343
QY 382 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 401
Db 1344 CAGGGTGACAGTGTGGGCCCTGTATGTACCAATCTGACCAAGTGGCATGTGTGGGCATC 1403
QY 402 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 421
Db 1404 GTTAGCTGGGGCTATGGCTGGGGGGCCGAGCACCCCGAGGAGTATACACCAAGGTCTCA 1463
QY 422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
Db 1464 GCCTATCTCACTGGATCTACATGTCTGGAAGGCTGAGCTG 1505

RESULT 15

US-10-006-130A-274
; Sequence 274, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.


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; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006.130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 274
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-130A-274

Alignment Scores:
Pred. No.:      8.51e-278      Length:      2063
Score:          2297.50        Matches:      429
Percent Similarity: 98.85%      Conservative: 0
Best Local Similarity: 98.85%      Mismatches: 0
Query Match:     98.10%      Indels:      5
DB:              12          Gaps:         1

US-09-607-745-2 (1-435) x US-10-006-130A-274 (1-2063)

QY      2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg 21
Db      219 GATCCTGACAGTGATCAACCTCTGAACAGCTCGATGCAAAACCCCTGGCGAAACCCCGT 278

QY      22 IleProMetGluThrPheArgLysValGlyLeuProIleIleIleAlaLeuLeuSerLeu 41
Db      279 ATCCCCATGGAGACCTTCAGAAAGTGGGGATCCCATCATAGCAGTACTACTGAGCCTG 338

QY      42 AlaSerIleIleIleValValValIleValIleValIleValIleValIleValIleVal 61
Db      339 GCGAGTATCATCTGTGGTGTCTCTCATCAAGGTGATCTGGATAAATATCTACTTCTCTC 398

QY      62 CysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCys 81
Db      399 TGGCGGAGCCCTCTCCACTTCATCCCGAGGAGCAGCTGTGTGACGGAGCTGGAGCTGTG 458

QY      82 ProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaValAla 101
Db      459 CCCTTGGGGAGGAGCAGAGGAGCACTGTGTCAAGAGCTTCCCGGAGGCGCTGCAGTGSCA 518

QY      102 ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp 121
Db      519 GTCCGCCTCTCCAGGACCGATCCACACTGCAGGGTGTGGACTCGGCCACAGGGAACCTGG 578

QY      122 PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMet 141
Db      579 TTCCTGCTGCTTTCGACAACTTCACAGAACTCTCGCTGAGACAGCCCTGTAGGCAGATG 638

QY      142 GlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAsp 161
Db      639 GGCTACAGC-----AGAGCTGTGGAGATTGGCCACAGACAGGATCTGGAT 683

QY      162 ValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCys 181
Db      684 GTTGTGAAATCACAGAAACACAGCCAGGAGCTTCGATCGCGAACTCAAGTGGGCCCTGT 743

QY      182 LeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPro 201
Db      744 CTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAAGAGAGCTGAGACACCCC 803

QY      202 ArgValValGlyGlyGluAlaSerValAspSerTrpProTrpGlnValSerIleGln 221
Db      804 CGTGTGGTGGTGGGAGGAGGAGCCCTCTGTGGATTCTTGGCCCTTGGCAGGTGAGCATCCAG 863

QY      222 TyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAla 241
Db      864 TACGCAAAACAGCAGCTCTGTGGAGGAGGAGCATCTTGGACCCCTCTGGGTCTCTACGGCA 923

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Search completed: December 2, 2003, 05:05:10
Job time : 422.82 secs

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QY      242 AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp 261
Db      924 GCCCATGCTTCAGGAAACATACCCGATGTGTCACTGGAGGTGGGGCAGGCTCAGAC 983

QY      262 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleLeuGluPheAsnPro 281
Db      984 AAACCTGGCAGCTTCCCATCCCTGGCTGTGGCCAGATCATCATCATGAATTCACACCCC 1043

QY      282 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 301
Db      1044 ATGTACCCCAAGACAAATGACATCGCCCTCATGAAGCTGAGTCCCATCTTCTCTCA 1103

QY      302 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 321
Db      1104 GGCACAGTCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1163

QY      322 LeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 341
Db      1164 CTCTGGATCATTTGGATGGGCTTTTACGAAGCAGATGGAGGAGATGTCTGCATACTG 1223

QY      342 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 361
Db      1224 CTGAGGCGTCAGTCCAGGTCAATTGACGACACGGTGCATGACAGCAGTGGTACCAG 1283

QY      362 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 381
Db      1284 GGGGAAAGTCACCCGAGAGATGATGTGTCAGGCGATCCCGGAGGGGTGTGGACACCTGC 1343

QY      382 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 401
Db      1344 CAGGGTGACAGTGGTGGGCCCTTGATGACCAATCTGACCAAGTGGCATGTGGTGGGCATC 1403

QY      402 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 421
Db      1404 GTTAGCTGGGGCTATGCTCGGGGGCCCGAGACCCCGAGGTATACCAAGGTCTCA 1463

QY      422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
Db      1464 GCCTATCTCAACTGGATCTACAAATGTCTGGAAGGCTGAGCTG 1505

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 2, 2003, 02:30:15 ; Search time 83.7689 Seconds
(without alignments)
2292.040 Million cell updates/sec

Title: US-09-607-745-2

Perfect score: 2342

Sequence: 1 MDPDSQPLNSLDVKPLRPK.....VTYKVSAYLNWYINWVKAEI 435

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries.

Command line parameters:

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-DB=Issued Patents NA -Qfmt=fastap -SUFFIX=tni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MAVRX=blsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US09607745@cgn_1_133 -runat_01122003_160938_9959 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2338	99.8	2038	3	US-09-008-271A-18
2	2324	99.2	2079	4	US-09-656-002-1
3	677.5	28.9	2479	3	US-09-342-749-29
4	677.5	28.9	2479	3	US-09-691-840-29
5	676.5	28.9	1479	3	US-09-342-749-1
6	676.5	28.9	1479	4	US-09-691-840-1
7	650.5	27.8	2413	3	US-09-518-046-1
8	627	26.8	2544	3	US-09-518-046-3
9	621.5	26.5	2416	3	US-09-261-416-1
10	584.5	25.0	1783	3	US-09-510-738A-188
11	584.5	25.0	1783	4	US-09-861-966-188
12	584.5	25.0	2363	4	US-09-742-703-3

13	580	24.8	1615	4	US-09-820-002-1	Sequence 1, Appli
14	578	24.7	1605	2	US-09-000-846-1	Sequence 1, Appli
15	576	24.6	1460	4	US-09-370-838-80	Sequence 80, Appl
16	576	24.6	1517	1	US-08-508-448C-15	Sequence 15, Appl
17	576	24.6	2790	4	US-09-370-838-79	Sequence 79, Appl
18	574	24.5	1462	4	US-09-370-838-55	Sequence 55, Appl
19	571	24.4	2581	1	US-08-200-900A-1	Sequence 1, Appli
20	571	24.4	2581	5	PCT-US94-00616-1	Sequence 1, Appli
21	558.5	23.8	1077	3	US-08-807-151-2	Sequence 2, Appli
22	558.5	23.8	1077	4	US-09-478-957-2	Sequence 2, Appli
23	531.5	22.7	696	1	US-08-508-448C-24	Sequence 24, Appl
24	516.5	22.1	901	1	US-08-508-448C-9	Sequence 9, Appli
25	503.5	21.5	959	4	US-09-023-942A-25	Sequence 25, Appl
26	496	21.2	1613	4	US-09-387-375-1	Sequence 1, Appli
27	483	20.6	1100	4	US-09-023-942A-5	Sequence 5, Appli
28	478	20.4	1081	3	US-09-008-271A-15	Sequence 15, Appl
29	477	20.4	1094	4	US-09-023-942A-3	Sequence 3, Appli
30	472.5	20.2	1430	4	US-09-386-629-1	Sequence 1, Appli
31	467.5	20.0	1110	4	US-09-386-653A-1	Sequence 1, Appli
32	466.5	19.9	1225	4	US-09-734-675-1	Sequence 1, Appli
33	463	19.8	3147	2	US-09-027-337-1	Sequence 1, Appli
34	463	19.8	3147	4	US-09-644-600-1	Sequence 1, Appli
35	463	19.8	3147	4	US-09-644-600-18	Sequence 18, Appl
36	462.5	19.7	980	4	US-09-023-942A-30	Sequence 30, Appl
37	462.5	19.7	1212	4	US-09-620-312D-431	Sequence 431, App
38	458.5	19.6	1130	4	US-09-387-375-8	Sequence 8, Appli
39	458	19.6	1739	2	US-08-861-151-2	Sequence 2, Appli
40	449.5	19.2	1165	4	US-09-023-942A-28	Sequence 28, Appl
41	445	19.0	933	4	US-09-023-942A-29	Sequence 29, Appl
42	443.5	18.9	1130	4	US-09-386-653A-8	Sequence 8, Appli
43	443	18.9	2296	1	US-07-750-080A-18	Sequence 18, Appl
44	443	18.9	2296	3	US-08-651-472-18	Sequence 18, Appl
45	443	18.9	2296	3	US-08-358-928-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-008-271A-18
; Sequence 18, Application US/09008271A
; Patent No. 6203979

; GENERAL INFORMATION:

APPLICANT: Bandman, Olga

Yue, Henry

Guegler, Karl J.

Corley, Neil C.

Tang, Tom Y.

Shah, Purvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/008,271A

FILING DATE: 16-Jan-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mohan-Peterson, Sheela

REGISTRATION NUMBER: 41,201

REFERENCE/DOCKET NUMBER: PF-0458 US

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Best Local Similarity: 99.77%      Mismatches: 0
Query Match:           99.23%      Indels: 1

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DB: 4 Gaps: 0
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QY 2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg 21
DB 217 GATCCTGACAGTGTATCAACTCTCTGAACAGCCTCGATGTCAAAACCCCTGGCGAAACCCCGT 276
QY 22 IleProMetGluThrPheArgLys-ValGlyIleProIleIleIleIleAlaLeuSerLe 41
DB 277 ATCCCCATGGAGACCTTCAGAAAGTGTGGGATCCCATCATCATAGCACTACTAGACCT 336
QY 41 uAlaSerIleIleIleValValValLeuIleLysValIleLeuAspLysTyrTrpPheLe 61
DB 337 GCGAGATATCATATGTGGTGTGCTCATCAAGTGATTCGATATAATCTACTTCTCT 396
QY 61 uCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGluLeuAspCy 81
DB 397 CTGCGGCGAGCCTCTCCACTTCATCCCGAGGAGCAGCTGTGTGACGGAGAGCTGGACTG 456
QY 81 sProLeuGlyGluAspGluHisCysValLysSerPheProGluGlyProAlaValAl 101
DB 457 TCCCTTGGGGAGAGCAGGAGCAGCTGTGTCAAGAGCTTCCCGAAGGGCCTGCAGTGGC 516
QY 101 aValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTr 121
DB 517 AGTCGGCTCTCCAGAGACCGATCCACACTGAGGTGTGACTCGGCCACAGGGAACTG 576
QY 121 pPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMe 141
DB 577 GTTCTCTGCTGTTTCGACAACTTCACAGAAAGCTCTGCTGAGACAGCCTGTAGGCAGAT 636
QY 141 tGlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAs 161
DB 637 GGGCTACAGCAGCAACCCATTTTCAGAGCTGTGGAGATTGCGCCAGACCAAGATCTGGA 696
QY 161 pValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCy 181
DB 697 TGTGTTGAATATCAGAAACAGCCAGAGCTTCGCATGCGGAACCTCAAGTGGGCCCTG 756
QY 181 sLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThrPr 201
DB 757 TCTCTCAGGCTCCCTGGTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 816
QY 201 oArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGl 221
DB 817 CCGTGTGTGGTGGGAGGAGGCTCTGTGATTCCTTGGCCCTTGGCAGGTGAGCATCCA 876
QY 221 nTyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAl 241
DB 877 GTACGACAAACAGCAGCAGTCTGTGGAGGGAGCATCTCGACCCCACTGGTCTCTCACGGC 936
QY 241 aAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAs 261
DB 937 AGCCCACTGCTTCAGAAACATACCGATGTGTCAACTGGAAGGTGCGGGCAGGCTCAGA 996
QY 261 pLysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPr 281
DB 997 CAATCTGGGAGCTTCCCATCCCTGGCTGTGGCCCAAGATCATCATTTGAATTCACACC 1056
QY 281 oMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSe 301
DB 1057 CATGTACCCCAAGACATGACATGCCCTCATGAAGTGTGAGTTCCTCCACTCCTTCTC 1116
QY 301 rGlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPr 321
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QY 321 oLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLe 341
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DB 1417 CGTAGCTGGGCTATGGCTGCGGGGCCCGAGCACCCAGAGGATATACACCAAGGTC 1476
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RESULT 3
US-09-342-749-29
; Sequence 29, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMRSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/342,749
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 60/091,044
; EARLIER FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 2479
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-342-749-29
Alignment Scores:
Pred. No.: 1,81e-63 Length: 2479
Score: 677.50 Matches: 151
Percent Similarity: 54.05% Conservative: 56
Best Local Similarity: 39.43% Mismatches: 127
Query Match: 28.93% Indels: 49
DB: 3 Gaps: 13
US-09-607-745-2 (1-435) x US-09-342-749-29 (1-2479)
QY 75 CysAspGlyGluLeuAspCysProLeuGlyGluAspGluHisCysValLysSerPhe 94
DB 453 TGTGATGCGCTGTACACACTGCCCCGGGGGAGGACGAGAATCGGTGTGTTCGCTCTAC 512
QY 95 ProGluGlyProAlaValAlaValArgLeuSerLysAspArgSerThrLeuGluValLeu 114
DB 513 -----GGACCA-----AACTCATCTTCAGATGTAC 539
QY 115 AspSerAlaThrGlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAla 134
DB 540 TCATCTCAGAGGAAGTCTTGGCCCTGTGTGCCAAGCAGCTGGAACGAGAACTACGGG 599
QY 135 GluThrAlaCysArgGlnMetGlyTyrSerSerLysProThrPheArgAlaValGluLe 154
DB 600 CGGCGCGCTCTCAGGGACATGGGCTAT-----AAGAATAATTTTACTCTAGCCAA--- 650
QY 155 GlyProAspGlnAspLeuAspValValGluLeuThrGluAsnSerGlnGluLeuArgMet 174
DB 651 -----GGAAATAGTGGATGACACGCGGATCCACCAAGCTTTTATGAAACTG 692
QY 175 ArgAsnSerSerGly-----ProCysLeu 182
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Db 693 AACCAAGTGGCGGCAATGTCGATATCTATATAAACTGTACCAAGCATGCTGTCT 752
Qy 183 SerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeu-----Lys 199
Db 753 TCAAAAGCAGTGGTTCCTTTACGCTGTTTAGCCTGCGGGGTCAACTTGAATCAAGCGC 812
Qy 200 ThrProArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSer 219
Db 813 CAGAGCAGATCGTGGCGGTGAGAGCGGCTCCCGGGGCTGCGCTGGCAGTCAAG 872
Qy 220 IleGlnTyrAspLysGlnHisValCysGlySerLeuLeuAspProHisTrpValLeu 239
Db 873 CTGCAGCTCCAGACGTCACGCTGTCGAGGCTCCATCATCACCCCGAGTGCATCGT 932
Qy 240 ThrAlaAlaHisCysPheArgLysHis---ThrAspValPheAsnTrpLysValArgAla 258
Db 933 ACAGCGCCCACTGGTGGAAAACTCTTAAACAATCCATGGCAATGGACGCAATTCGG 992
Qy 259 GlySerAspLysLeuGlySerPhe-----ProSerLeuAlaValAlaLysIle 274
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Qy 292 MetLysLeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhe 311
Db 1101 ATGAAGCTGCAGAAAGCTCTGACTTTTCAACGACCTAGTGAACCAAGTGTCTGCCCAAC 1160
Qy 312 PheAspGluGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLys 331
Db 1161 CCAGGCATGATGCTGACGACGACAGACAGCTCTGCTGATTTCCGGTGGGGGCCACCGAG 1220
Qy 332 GlnAsnGlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSer 351
Db 1221 GAGAAA---GGGAAGACCTCAGAAGTGTGACGCTGCCAAGGTGCTTCTCATTTGAGACA 1277
Qy 352 ThrArgCysAsnAlaAspAlaTyrGlnGlyGluValThrGlnLysMetMetCysAla 371
Db 1278 CAGAGATGCAACAGCAGATATGCTATGACAACTCATCACACCCATGATCTGTGCC 1337
Qy 372 GlyIleProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyr 391
Db 1338 GGTCTCTGCGGGGAGCTGCGATCTTCCAGGGTGACAGTGGAGGCTCTGGTCACT 1397
Qy 392 GlnSerAspGln---TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGly 410
Db 1398 TCGAACAAACAATATCTGCTGGCTGATAGGGGATACAAAGCTGGGGTCTGGCTGGCCAAA 1457
Qy 411 ProSerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyrAsnVal 430
Db 1458 GCTTACAGACGAGGTGACGGGAATGTGATGTTATTCAGGACTGGAATTTATCGACAA 1517
Qy 431 TrpLysAla 433
Db 1518 ATGAAGCA 1526
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RESULT 4

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US-09-691-840-29
; Sequence 29, Application US/09691840
; Patent No. 644419
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMPS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/691,840
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US/09/342,749
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; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/091,044
; PRIOR FILING DATE: 1998-06-29
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; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
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; LENGTH: 2479
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-691-840-29
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Alignment Scores:

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Pred. No.: 1.81e-63 Length: 2479
Score: 677.50 Matches: 151
Percent Similarity: 54.05% Conservative: 56
Best Local Similarity: 39.43% Mismatches: 127
Query Match: 28.93% Indels: 49
DB: 4 Gaps: 13
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US-09-607-745-2 (1-435) x US-09-691-840-29 (1-2479)
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Qy 75 CysAspGlyGluLeuAspCysProLeuGlyGluAspGluHisCysValLysSerPhe 94
Db 453 TGTGATGGCTGTCTACACTGCCCCGCGGGGAGGACGAGATCGGTGTGTTCCGCTCTAC 512
Qy 95 ProGluGlyProAlaValAlaValArgLeuSerLysAspArgSerThrLeuGlnValLeu 114
Db 513 -----GGACCA-----AACTTCATCTCTCAGATGTAC 539
Qy 115 AspSerAlaThrGlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAla 134
Db 540 TCATCTCAGAGAAAGTCTCTGGCACCCCTGTGTGCCAAGACGACTGGAAACGAGAACTACGGG 599
Qy 135 GluThrAlaCysArgGlnMetGlyTy-SerSerLysProThrPheArgAlaValGluIle 154
Db 600 CGGGCGGCTGTCAGGACATGGCTAT-----AAGATAATTTTACTCTAGCCAA--- 650
Qy 155 GlyProAspGlnAspLeuAspValValGluIleThrGluAsnSerGlnGluLeuArgMet 174
Db 651 -----GGATAGTGGATGACAGCGGATCCACGAGCTTTATGAACTG 692
Qy 175 ArgAsnSerSerGly-----ProCysLeu 182
Db 693 AACACAAGTGGCGGAATTCGATATCTATAAAACTGTATACCAAGATGCTGTCTTCT 752
Qy 183 SerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeu-----Lys 199
Db 753 TCAAAAGCAGTGGTTCCTTTACGCTGTTTAGCCTGCGGGGTCAACTTGAACCTCAAGCCGC 812
Qy 200 ThrProArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSer 219
Db 813 CAGAGCAGATCGTGGCGGTGAGAGCGGCTCCCGGGGCTGCGCTGGCAGTCAAG 872
Qy 220 IleGlnTyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeu 239
Db 873 CTGCAGCTCCAGACGTCACGCTGTCGAGGCTCCATCATCACCCCGAGTGCATCGT 932
Qy 240 ThrAlaAlaHisCysPheArgLysHis---ThrAspValPheAsnTrpLysValArgAla 258
Db 933 ACAGCGCCCACTGGTGGAAAACTCTTAAACAATCCATGGCAATGGACGCAATTCGG 992
Qy 259 GlySerAspLysLeuGlySerPhe-----ProSerLeuAlaValAlaLysIle 274
Db 993 GGGATTTTCAGA---CAATCTTTTCATGTTCTATGGAGCGCGATACCAAGTCAAAAAGTG 1049
Qy 275 IleIleIleGluPheAsnProMetTyr-----ProLysAspAsnAspIleAlaLeu 291
Db 1050 ATT-----TCTCATCCAAATTATGACTCCCAAGACCAAGACAATGACATTGCGCTG 1100
Qy 292 MetLysLeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhe 311
Db 1101 ATGAAGCTGCAGAAAGCTCTGACTTTTCAACGACCTAGTGAACCAAGTGTCTGCCCAAC 1160
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QY 312 PheAspGluLeuThrProAlaThrProLeuTrrPilleGlyTrpGlyPheThrLys 331
Db 1161 CCAGGATGATCTGCGAGCAGACAGCTCTCTGATTCGGGTGGGGGCCACCGAG 1220
QY 332 GlnAsnGlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSer 351
Db 1221 GAGAAA---GGAGAGACCTCAGAGTCTGAAGCTGCCAAGGTCTCTCTATTGAGACA 1277
QY 352 ThrArgCysAsnAlaAspAlaTyrGlnGlyGluValThrGluLysMetMetCysAla 371
Db 1278 CAGAGATGCAACAGCAGATATGCTATGACAACCTGATCACCAGCCATGATCTGTGCC 1337
QY 372 GlyIleProGluGlyClyValAspThrCysGlnGlyValSerTrpGlyTyrGlyGly 391
Db 1338 GGCCTCTCTCGAGGGGAACCTGATCTTCCAGGGTGACAGTGGAGGGCTCTGGTCACT 1397
QY 392 GlnSerAspGln---TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGly 410
Db 1398 TCGAACACAATATCTGGTGGCTGATAGGGGATACAGCTGGGTCTGGCTGCCAAA 1457
QY 411 ProSerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyrAsnVal 430
Db 1458 GCTTACAGACAGGAGTACGGGAATGTGATGTATTCCAGGACTGGATTTATCGACAA 1517
QY 431 TrpLysAla 433
Db 1518 ATGAGGCA 1526

RESULT 5
US-09-342-749-1
/ Sequence 1, Application US/09342749
/ Patent No. 6166194
/ GENERAL INFORMATION:
/ APPLICANT: Wong, Alexander K.C.
/ APPLICANT: Tavtigian, Sean V.
/ APPLICANT: Teng, David H.-F.
/ APPLICANT: Myriad Genetics, Inc.
/ TITLE OF INVENTION: TMPS22 is a Tumor Suppressor
/ FILE REFERENCE: 2318-202
/ CURRENT APPLICATION NUMBER: US/09/342,749
/ CURRENT FILING DATE: 1999-06-29
/ EARLIER APPLICATION NUMBER: US 60/091,044
/ EARLIER FILING DATE: 1998-06-29
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 1479
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1476)
/ FEATURE:
/ NAME/KEY: conflict
/ LOCATION: (724)
/ OTHER INFORMATION: Listed as T in GenBank Accession No. U75329
/ FEATURE:
/ NAME/KEY: conflict
/ LOCATION: (985)
/ OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329
/ FEATURE:
/ NAME/KEY: conflict
/ LOCATION: (1347)
/ OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329
/ FEATURE:
/ NAME/KEY: conflict
/ LOCATION: (1466)
/ OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329
/ FEATURE:
/ NAME/KEY: conflict
/ LOCATION: (1471)
/ OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329.
/ FEATURE:
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/ NAME/KEY: allele
/ LOCATION: (478)
/ OTHER INFORMATION: This base can be G or A with G being the more
/ OTHER INFORMATION: common allele. The codon will change from Val to
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (777)
/ OTHER INFORMATION: This base can be C or T with C being the more
/ OTHER INFORMATION: common allele. The codon is unaffected with both
/ OTHER INFORMATION: alleles encoding Gly.
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (768)
/ OTHER INFORMATION: This base can be C or T with C being the more
/ OTHER INFORMATION: common allele. This is a silent polymorphism.
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (834)
/ OTHER INFORMATION: This base can be C or T with C being the more
/ OTHER INFORMATION: common allele. This is a silent polymorphism.
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (625)
/ OTHER INFORMATION: This base can be T or A with T being the more
/ OTHER INFORMATION: common allele. The codon will change from Phe to
/ OTHER INFORMATION: Ile
US-09-342-749-1

Alignment Scores:
Pred. No.: 1,04e-63 Length: 1479
Score: 676.50 Matches: 150
Percent Similarity: 53.91% Conservative: 57
Best Local Similarity: 39.06% Mismatches: 128
Query Match: 28.89% Indels: 49
DB: Gaps: 13

US-09-607-745-2 (1-435) x US-09-342-749-1 (1-1479)
QY 75 CysAspGlyGluLeuAspCysProLeuGlyGluAspGluGluHisCysValLysSerPhe 94
Db 397 TGTGATGGGTGTCTACACTGCCCGGGGAGGACGAGAAATCGGTGTGTTCGCTCTAC 456
QY 95 ProGluGlyProAlaValAlaValArgLeuSerLysAspArgSerThrLeuGlnValLeu 114
Db 457 -----GGACCA-----AACTTCATCTTCAGGTGTAC 483
QY 115 AspSerAlaThrGlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAla 134
Db 484 TCATCTCAGAGGAAGTCTGGCACCCCTGTGTGCCAAGACGACTGGAACGAGAACTACGGG 543
QY 135 GluThrAlaCysArgGlnMetGlyTyrSerSerLysProThrPheArgAlaValGluIle 154
Db 544 CGGGCGGCTGCGAGGACATGGGCTAT-----AAGAAATAATTTTACTTACGCCAA--- 594
QY 155 GlyProAspGlnAspLeuAspValValGluIleThrGluAsnSerGlnGluLeuArgMet 174
Db 595 -----GGATAGTGATGACAGCGGATCCACCAGCTTATGAAACTG 636
QY 175 ArgAsnSerSerGly-----ProCysLeu 182
Db 637 AACACAAGTCCCGCAATGTCGATATCTATAAAAACTGTACCACAGTGTGCTGTCT 696
QY 183 SerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeu-----Lys 199
Db 697 TCAAAAGCAGTGTGTTCTTTTACGCTGTATAGCTCGGGGTCAACTTGAACCTCAAGCCGC 756
QY 200 ThrProArgValValGlyGluGluAlaSerValAspSerTrpProTrpGlnValSer 219
Db 757 CAGAGCAGGATCTGTGGCGCGGAGCGCCCTCCCGGGGCCCTGGCCCTGCGAGGTGAGC 816
QY 220 IleGlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeu 239
Db ::::
```

Db 817 CTGCGCTCCAGACGTCACCGTGTGGGAGGCTCCATCATCACCCCGAGTGGATCGTG 876
Qy 240 ThrAlaAlaHisCysPheArgLysHis---ThrAspValPheAsnTrpLysValArgAla 258
Db 877 ACAGCGCCGACCTGGTGGAAAAAAGCTCTTAACATCCATGGCATGGACGCATTGGCG 936
Qy 259 GlySerAspLysLeuGlySerPhe-----ProSerLeuAlaValAlaLysIle 274
Db 937 GGGATTTCAGAA---CAATCTTTTCATGTTCTATGGAGCCGGATACCAAGTAGAAAAAGTG 993
Qy 275 IleIleIleGluPheAsnProMetTyr-----ProLysAspAsnAspIleAlaLeu 291
Db 994 ATT-----TCTCATCCAAATTATGACTCCAGAACCAAGAACATGACATTCGGCTG 1044
Qy 292 MetLysLeuGluPheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhe 311
Db 1045 ATGAAGCTGACAGAGCCTCTGACTTTCAACGACCTAGTGAACACCATGTGTCTGCCCAAC 1104
Qy 312 PheAspGluGluLeuThrProLalaThrProLeuTrpIleIleGlyTrpGlyPheThrLys 331
Db 1105 CCAGGCGATGATGTCGAGCCAGAACAGCTCTGCTGGATTTCGGGTGGGGGCCACCGAG 1164
Qy 332 GlnAsnGlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSer 351
Db 1165 GAGAAA---GGGAAGACCTCAGAGTGCTGAACGCTGCCAAGGTCTTCTCATTTAGACA 1221
Qy 352 ThrArgCysAsnAlaAspAlaTrpGlnGlyGluValThrGluLysMetMetCysAla 371
Db 1222 CAGAGATGCAACAGCAGATATGCTATGACCACTGATCACACCGCATGATCTGTGCC 1281
Qy 372 GlyIleProGluGlyValAspThrCysGlnGlyAspSerGlyCysProLeuMetTyr 391
Db 1282 GCGTCTCTCCAGGGGAACCTCGATTCTGCCAGGTGACAGTGGAGGGCTCTGTGCTCACT 1341
Qy 392 GlnSerAspGln---TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGly 410
Db 1342 TCGAAGAACAAATCTGGTGGCTGATGAGGGGATACAGCTGGGGTCTGGCTGTGCCAAA 1401
Qy 411 ProSerThrProGlyValTrpThrLysValSerAlaTrpLeuAsnTrpIleTyrAsnVal 430
Db 1402 GCTTACAGACAGGAGTGTACGGGATGTGATGTATTTCAGGACTGGATTATCGACAA 1461
Qy 431 TrpLysAlaGlu 434
Db 1462 ATGAGGGCAGAC 1473

RESULT 6
US-09-691-840-1
Sequence 1, Application US/09691840
Patent No. 6444419
GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.-F.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: TMRSS2 is a Tumor Suppressor
FILE REFERENCE: 2318-202
CURRENT APPLICATION NUMBER: US/09/691,840
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: US/09/342,749
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 60/091,044
PRIOR FILING DATE: 1998-06-29
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1479
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1..(1476))
NAME/KEY: conflict

LOCATION: (724)
OTHER INFORMATION: Listed as T in GenBank Accession NO. U75329
NAME/KEY: conflict
LOCATION: (985)
OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
NAME/KEY: conflict
LOCATION: (1347)
OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
NAME/KEY: conflict
LOCATION: (1466)
OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329
NAME/KEY: conflict
LOCATION: (1471)
OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329
NAME/KEY: allele
LOCATION: (478)
OTHER INFORMATION: This base can be G or A with G being the more common allele. The codon will change from Val to Met.
NAME/KEY: allele
LOCATION: (777)
OTHER INFORMATION: This base can be C or T with C being the more common allele. The codon is unaffected with both
OTHER INFORMATION: alleles encoding Gly.
NAME/KEY: allele
LOCATION: (768)
OTHER INFORMATION: This base can be C or T with C being the more common allele. This is a silent polymorphism.
NAME/KEY: allele
LOCATION: (834)
OTHER INFORMATION: This base can be C or T with C being the more common allele. This is a silent polymorphism.
NAME/KEY: allele
LOCATION: (625)
OTHER INFORMATION: This base can be T or A with T being the more common allele. The codon will change from Phe to Ile
US-09-691-840-1

Alignment Scores:
Pred. No.: 1,04e-63 Length: 1479
Score: 676.50 Matches: 150
Percent Similarity: 53.91% Conservative: 57
Best local Similarity: 39.06% Mismatches: 128
Query Match: 28.89% Indels: 49
DB: 4 Gaps: 13

US-09-607-745-2 (1-435) x US-09-691-840-1 (1-1479)

Qy 75 CysAspGlyGluLeuAspCysProLeuGlyGluAspGluHisCysValLysSerPhe 94
Db 397 TGTGATGGCGTGTCACTGCCCCGGGGGAGGACGAGAAATCGGTGTGTTCGCTCTAC 456
Qy 95 ProGluGlyProAlaValAlaValArgLeuSerLysAspArgSerThrLeuGlnValLeu 114
Db 457 -----GGACCA-----AAGTTCATCTCTTCAGGTGTAC 483
Qy 115 AspSerAlaThrGlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAla 134
Db 484 TCATCTCAGAGGAAGTCTCGCACCTGTGTGCCAAGACGATCGGACGAGAACTACGGG 543
Qy 135 GluThrAlaCysArgGlnMetGlyTyrSerSerLysProThrPheArgAlaValGluIle 154
Db 544 CGGGCGGCTCGAGGACATGGCTAT-----AAGATAATTTTCTACTAGCCAA--- 594
Qy 155 GlyProAspGlnAspLeuAspValValGluIleThrGluAsnSerGlnGluLeuArgMet 174
Db 595 -----GGAATAGTGTATCAGCGGATCCACCAGCTTTATGAACTG 636
Qy 175 ArgAsnSerSerGly-----ProCysLeu 182
Db 637 AACACAAGTGGCGGAAGTTCGATATCTATAAAAGTACACAGTATGCTGTCT 696
Qy 183 SerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeu-----Lys 199

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Db      697 TCAAGAGCAGTGGTTCTTACGCTGTATAGCTCGGGTCACTTGAATCAGCGGC 756
Qy      200 ThrProArgValValGlyGlyGluLalaserValAspSerTrpTrpGlnValSer 219
Db      757 CAGACGAGTGTGGGGGGGAGAGCGGCTCCCGGGGGCTGGCCCTGGCAGGTGAGC 816
Qy      220 IleGlnTyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeu 239
Db      817 CTGACGCTCCAGAGCTCCAGCTGTGGAGGCTCCATCATCACCCCGAGTGGATCGTG 876
Qy      240 ThrAlaAlaHisCysPheArgLysHis---ThrAspValPheAsnTrpLysValAlaGala 258
Db      877 ACAGCGCCCACTGCTGGTGGAAAACTCTTAACAATCCATGCAATGGACGGCAATTGG 936
Qy      259 GlySerAspLysLeuGlySerPhe-----ProSerLeuAlaValAlaLysIle 274
Db      937 GGGATTTTGAGA---CAATCTTTTCATGTCTATGAGCGCGGATACCAAGTGAAGAAAGTG 993
Qy      275 IleIleIleGluPheAsnProMetTyr-----ProLysAspAsnAspIleAlaLeu 291
Db      994 ATT-----TCTCATCCAAATTAAGACTCCAGACCAAGAACATGACATTCGGCTG 1044
Qy      292 MetLysLeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhe 311
Db      1045 ATGAAGCTGCAGAGCCTCTGACTTTCACGACCTAGTAGAACCACTGTGTGCCCCAAC 1104
Qy      312 PheAspGluGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLys 331
Db      1105 CCAGGCATGATGCTCCAGCCAGAACAGCTCTCTCTGGATTTCGGGTGGGGGCCACCGAG 1164
Qy      332 GlnAsnGlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSer 351
Db      1165 GAGAAA---GGGAACACCTCAGAAGTGTGACGCTGCCAGGTCTCTCATTTAGACA 1221
Qy      352 ThrArgCysAsnAlaAspAlaTyrGlnGlyGluValThrGluLysMetMetCysAla 371
Db      1222 CAGAGATGCAACAGCAGATATGCTATGACACACCTGATCAGACCCAGCCATGATGTGCC 1281
Qy      372 GlyIleProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyr 391
Db      1282 GGTCTTCCTGAGGGGAACGTCCGATTTCTTCCAGGGTGACAGTGGAGGGCCCTGTGTCACT 1341
Qy      392 GlnSerAspGln---TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGly 410
Db      1342 TCGAAGACAATATCTGTGCTGTATAGGGGATACAGCTGGGGTCTGGCTGTGCCAAA 1401
Qy      411 ProSerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyrAsnVal 430
Db      1402 GCTTACAGACCAAGGAGTGTACGGGAATGTGATGATTCAAGGACTGGATTATCGACAA 1461
Qy      431 TrpLysAlaGlu 434
Db      1462 ATGAGGGCAGAC 1473

```

RESULT 7

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US-09-518-046-1
; Sequence 1, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 1
; LENGTH: 2413
; TYPE: DNA

```

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 gene
US-09-518-046-1

```

Alignment Scores:

```

Pred. No.: 1,49e-60 Length: 2413
Score: 650.50 Matches: 157
Percent Similarity: 52.14% Conservative: 74
Best Local Similarity: 35.44% Mismatches: 149
Query Match: 27.78% Indels: 63
DB: 3 Gaps: 18

```

US-09-607-745-2 (1-435) x US-09-518-046-1 (1-2413)

```

Qy      22 IleProMetGlnThrPheArgLysValGlyIleProIleIleAlaLeuSerLeu 41
Db      273 CTGCCATTGAAGTTTTCCTCAATCATCGTCATTGGGGATCATTCGATTG----- 323
Qy      42 AlaSerIleIleValValValLeuIleLysValIleLeuAsp-----LysTyr 58
Db      324 -----ATATTAGCACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTAC 377
Qy      59 -----TyrPheLeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeu 74
Db      378 AGATGTCGCTCATCCTTTAAGTGT-----ATCGAGCTGATAACTCGA----- 419
Qy      75 CysAspGlyGluLeuAspCysProLeuGlyGluAspGluGluHisCysValLysSerPhe 94
Db      420 TGTGACGGAGTCTCGGATTGCCAAGACGGGAGGACGAGTACCGCTGT----- 467
Qy      95 ProGluGlyProAlaValAlaValArgLeuSerLysAspArgSerThrLeuGlnValLeu 114
Db      468 -----GTCCGGGTGGGTGCTCAGAAATGGTGTCTCCAGGTGTC 506
Qy      115 AspSerAlaThrGlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAla 134
Db      507 ACACCTGCT-----TCGTGGAACACCATGTCTCCGATGACTGGAAGGGTCACTACGCA 560
Qy      135 GluThrAlaCysArgGlnMetGlyTyrSerSer----- 145
Db      561 AATGTTGCTGTGCCAACCTGGGTTTCCCAAGCTATGTGAGTTTCAGATAACCTCAGAGTG 620
Qy      146 -----LysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuVal 162
Db      621 AGCTCGCTGGAGGGCGAGTTCGGGAGGAGTGTGTCTCCATCGATCACTCTTGCAGAT 680
Qy      163 ValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCysLeu 182
Db      681 GACAGGTGACTGCTATACACCACTCAGTATATGTGAGGGAGGA-----TGTGCC 731
Qy      183 SerGlySerLeuValSerLeuHisCysLeuAlaCysGly---LysSerLeuLysThrPro 201
Db      732 TCTGGCCACGTTGTTACCTTGCAGTGCACAGCCCTGTGTGTATAGAGGGGTGTACAGTCA 791
Qy      202 ArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGln 221
Db      792 CGCATCGTGGGTGGAACATGTCTCTCGCAGTGGCCCTCGCCAGCCAGCCAGCCTTCAG 851
Qy      222 TyrAspLysGlnHisValCysGlySerIleLeuAspProHisTrpValLeuThrAla 241
Db      852 TTCAGGGCTACCACTGTGGGGGGTCTGTGTATCATCGCCCTCTGTGATCATCACTGCT 911
Qy      242 AlaHisCysPheArgLysHisThrAspValPhe-----AsnTrpLysValAlaGala 258
Db      912 GCACACTGTGTT-----TATGACTGTGTACCTCCCAAGTCACTGACCATCCAGGTG 962
Qy      259 GlySerAspLysLeu-----GlySerPheProSerLeuAlaValAlaLysIleIle 276
Db      963 GGTCTAGTTTCCCTGTGGACAATCCAGCCCACTCCCACTTGGTGGAGAGATTGTC--- 1019
Qy      277 IleGluPheAsnProMetTyr---ProLys-----AspAsnAspIleAlaLeuMetLys 293

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1020	Db	-----TACCACAGCAGAGTAAAGCCAAAGAGCGGTGGGCAATGACATCGCCCTTATGAAG	1073
294	QY	LeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhePheAsp	313
1074	Db	CTGGCGGGGCATCTCAGCTTCATGAAATGATCAGCGCTGTGCCTGCCCAACTCTGAA	1133
314	QY	GlulGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsn	333
1134	Db	GAGAACTTCCCCGATGGAAAAAGTGTGTCGACGTCAGATGGGGGGCCACA--GAGGAT	1190
334	QY	GlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSerThrArg	353
1191	Db	GGAGGTGACCCCTCCCTGTCCTGAACACCGCGCGCGCTGCTTGATTTCCACAAGATC	1250
354	QY	CysAsnAlaAspAlaThrGlnGlyGluValThrGluLysMetMetCysAlaGlyIle	373
1251	Db	TGCAACACAGGACGTTACGGTGGGATCATCTCCCCCTCCATGCTCTCGGGGGGCTAC	1310
374	QY	ProGluGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrglnSer	393
1311	Db	CTACGGGTGGCTGGAACAGCTGCCAGGGGGACAGCGGGGGGCCCTCGGTGTGTCAAGAG	1370
394	QY	AspGln---TrpHisValValGlyIleValSerTrpGlyTyrglyCysGlyGlyProSer	412
1371	Db	AGAGGCTGTGGAAGTTAGTGGGAGCCACAGCTTTTGGCATTCGGCTCGGCAGAGGTGAAC	1430
413	QY	ThrProGlyValTyThrLysValSerAlaTyrrLeuAsnTrpIleTyrrAsnValTrpLys	432
1431	Db	AAGCTTGGGGTGATACACCCGTGTACACCTCTCTCTGGACTGGATCCACGAGCAGATGGAG	1490
433	QY	AlaGluLeu	435
1491	Db	AGAGACCTA	1499

RESULT 8

```

US-09-518-046-3
; Sequence 3, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; IN Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 3
; LENGTH: 2544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 variant gene
US-09-518-046-3

```

Alignment Scores:		
Pred. No.:	5,759-58	2544
Score:	627.00	Matches: 160
Percent Similarity:	48.14%	Conservative: 73
Best Local Similarity:	33.06%	Mismatches: 150
Query Match:	26.77%	Indels: 102
DB:	3	Gaps: 18

US-09-607-745-2 (1-435) x US-09-518-046-3 (1-2544)

Qy	22 IleProMetGluThrPheArgLysValGlyIleProIleIleIlealaLeuLeuSerLeu 41 ::: :
Db	273 CTGGCATTGAAGATTTTTCCCAATCATCGTCATTGGGGATCATTTGCATTG----- 323

Qy	42	AlaSerIleIleIleValValValValLeuIleLysValIleLeuAsp-----LysTyr	58
Db	324	-----ATATTAGCACTGGCCATTGCTCTGGGCAATCCACTTCGACTCTCAGGGAAGTAC	377
Qy	59	-----TyrPheLeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeu	74
Db	378	AGATGTCGCTCATCCCTTTAAGTGT-----ATCGAGCTGATAACTCGA-----	419
Qy	75	CysAspGlyGluLeuAspCysProLeuGlyGluAspGluGluHisCysValLysSerPhe	94
Db	420	TGTGACGGAGTCTCGATTGCAAGACGGGGAGGACGAGTACCGCTGT-----	467
Qy	95	ProGluGlyProAlaValAlaValArgLeuSerLysAspArgSerThrLeuGlnValLeu	114
Db	468	-----GTCCGGTGGGTGGTCAAGATCCGCTGCTCCAGGTGTTTC	506
Qy	115	AspSerAlaThrGlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAla	134
Db	507	ACAGCTGCT-----TCGTGGAAAGACATGTGCTCGGATGACTGAGGAAGGCTCACTACGCA	560
Qy	135	GluThrAlaCysArgGlnMetGlyTyrSerSer-----	145
Db	561	AATGTTGCCTGTGCCCAACCTGGGTTCCCAAGCTATGTAAGTTCAGATAACCTCAGAGTG	620
Qy	146	-----LysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAspVal	162
Db	621	AGTCGTGTGCGGGGCGGACCTTCGGGAGGAGTTTGTCTCCATCATCACCTCTTTCGCAGAT	680
Qy	163	ValGluIleThrGluAsnSerGlnGluLeuAsgMetArgAsnSerSerGlyProCysLeu	182
Db	681	GACAAGTGACTGCATTACCACTCAGTATATGTGAGGGAGGGA-----	731
Qy	183	SerGlySerLeuValSerLeuHisCysLeuAlaCysGly-----LysSerLeuLysThrPro	201
Db	732	TCTGGCACGTGTTTACCTTGAGTGCAGACGCTGTGTCATGAGAGGGCTACAGTCA	791
Qy	202	ArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGln	221
Db	792	CGCATCGTGGTGGAAACATGCTCTTGCTCTCGCAGTGGCCCTGGCAGGCGCAGCTTCAG	851
Qy	222	TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla	241
Db	852	TTCACAGGGCTACCACCTGTGCGGGGCTGTGCATCAGCCCTGTGGATCATCACTGCT	911
Qy	242	AlaHis-----	243
Db	912	GCACACTGTGTTTATGAGATTGTAGCTCTAGAGAAGGGCAGACAGAGAGGAAG	971
Qy	244	-----CysPheArgLysHisThrAspValPhe-----	252
Db	972	CTCCTGTGCTGGAGGAAACCCACAAAAATGAA-AGGACCTAGACCTTCCCATAGCTAATT	1030
Qy	253	-----	257
Db	1031	CCAGTGGACCATGTTATGGCAGATACAGGCTTGTACTCCCAAGTCATGAGCATTCACAG	1090
Qy	258	AlaGlySerAspLysLeu-----GlySerPheProSerLeuAlaValAlaLysIleIle	275
Db	1091	GTGGGTCTAGTTCCTCTGTGGCAATCCAGCCCCATCCCACTGTGTGGAGAGATTGTC	1150
Qy	276	IleIleGluPheAsnProMetTyr-----ProLys-----AspAsnAspIleAlaLeuMet	292
Db	1151	-----TACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATG	1201
Qy	293	LysLeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhePhe	312
Db	1202	AAGCTGCGGGGCACTCAGTTCAATGAATATCCAGGCTGTGTGCTGCCCAACTCT	1261
Qy	313	AspGluGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLysGln	332
Db	1262	GAGAGCAAGACTTCCCCGATGGAAAAGTGTGTGACGCTCAGGATGGGGGGCCACA---GAG	1318
Qy	333	AsnGlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSerThr	352

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Db 1319 GATGAGGTGACGCTCCCTCCCTGCTCTGAAACACGCGCGCGCTCTTTGATTTCACAAAG 1378
Qy 353 ArgCysAsnAlaAspAspAlaTyrGlnGlyValThrGluLysMetMetCysAlaGly 372
Db 1379 ATCTGCAACACACAGGACGCTGACGGTGGCATCATCTCCCTCCATGCTCTGCGCGGC 1438
Qy 373 IleProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGln 392
Db 1439 TACCTGACGGGTGGCTGGAGAGCTGCGCGGACACGCGGGGGCCCTGGTGTGTCAA 1498
Qy 393 SerAspGln---TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyPro 411
Db 1499 GAGAGGAGGCTGTGCAAGCTTAGTGGAGCGACCGAGCTTGGCATCGGCTGGCAGAGTG 1558
Qy 412 SerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyrAsnValTrp 431
Db 1559 AACAGGCTGGGGTGTACCCGCTGTACCTCTCTCTGGTGTGATCCACGAGCATG 1618
Qy 432 LysAlaGluLeu 435
Db 1619 GAGAGACCTA 1630

RESULT 9
US-09-261-416-1
; Sequence 1, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: TAGD-12: A No. 6291663el Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 144..1511
; OTHER INFORMATION: CDS
US-09-261-416-1

Alignment Scores:
Pred. No.: 2,1e-57 Length: 2416
Score: 621.50 Matches: 158
Percent Similarity: 51.57% Conservative: 72
Best Local Similarity: 35.43% Mismatches: 150
Query Match: 26.54% Indels: 66
DB: 3 Gaps: 18

US-09-607-745-2 (1-435) x US-09-261-416-1 (1-2416)
Qy 22 IleProMetGluThrPheArgLysValGlyIleProIleIleAlaLeuSerLeu 41
Db 273 CTGCCATTGAGTTTTTCCCAATCATCGTCATTTGGGATCATTCATTG----- 323
Qy 42 AlaSerIleIleValValValValLeuLeuLeuValIleLeuAsp-----LysTyr 58
Db 324 -----ATATTAGCACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAATAC 377
Qy 59 -----TyrPheLeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeu 74
Db 378 AGATCTCGCTCATCTCTTTAAGTGT-----ATCGAGCTGATAACTCGA----- 419
Qy 75 CysAspGlyGluLeuAspCysProLeuGlyGluAspGluGluHisCysValLysSerPhe 94
Db 420 TGTGACGAGTCTCGATTGCAAGACGGGAGGACGAGTACCGCTGT----- 467
Qy 95 ProGluGlyProAlaValAlaValArgLeuSerLysAspArgSerThrLeuGlnValLeu 114

```

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Db 468 -----GTCCGGTGGTGGTTCAGAAATGCGCTGCTCCAGGTGTC 506
Qy 115 AspSerAlaThrGlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAla 134
Db 507 ACAGCTGCT-----TCGTGGAAGACCATGTGCTCCGATGACTGGAAGGTCACATACGCA 560
Qy 135 GluThrAlaCysArgGlnMetGlyTyrSerSer----- 145
Db 561 AATGTTGCCTGTGCCCACTGGGTTTCCCAAGCTATGTGAGTTTCAGATAACCTCAGAGTG 620
Qy 146 -----LysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAspVal 162
Db 621 AGCTCGCTGAGGGGCGAGTTCCGGAGGAGTTTGTGTCCATCGATCACCCTCTCCAGAT 680
Qy 163 ValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCysLeu 182
Db 681 GACAAGGTGACTGATTTACACCTACCTAGTATATGTGAGGGAGGGA-----TGTGCC 731
Qy 183 SerGlySerLeuValSerLeuHisCysLeuAlaCysGly---LysSerLeuLysThrPro 201
Db 732 TCTGCCACAGTGTGTACCTTCAGTGCAGCCCTGTGTCTATAGAAGGGGCTACAGTCA 791
Qy 202 ArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGln 221
Db 792 CGCATCGTGGTGGAAACATGCTCTCTCGCAGTGGCCCTGCGCAGGCGCAGCCTTCAG 851
Qy 222 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 241
Db 852 TTCAGGGCTACCACTGTGCGGGGCTGTGTATCATCGCCCTGTGGATCATCAGTGTCT 911
Qy 242 AlaHisCysPheArgLysHisThrAspValPhe-----AsnTrpLysValArgAla 258
Db 912 GCACACTGTGTT-----TATGACTTGTACCTCCCAAGTCATGAGCACCATCCAGTG 962
Qy 259 GlySerAspLysLeu-----GlySerPheProSerLeuAlaValAlaIleIleIle 276
Db 963 GGTCTAGTTTCCCTGTTGGCAATCCAGCCCATCCCACTTGTGTGGAGAGATTGTT--- 1019
Qy 277 IleGluPheAsnProMetTyr---ProLys-----AspAsnAspIleAlaLeuMetLys 293
Db 1020 -----TACCACAGCAAGTACAAAGAGGCTGGGCAATGATCATCGCTGTGCTGCCCTTATGAAG 1073
Qy 294 LeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhePheAsp 313
Db 1074 CTGCCCGGGCCACTCAGCTTCATGAATGATCATCAGCTGTGCTGCTGCCCTTATGAAG 1133
Qy 314 GluGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsn 333
Db 1134 GAGAACTTCCCGATGGAAAAGTGTGCTGGACGTGAGGATGGGGGGCCACA---GAGGAT 1190
Qy 334 GlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSerThrArg 353
Db 1191 GGAGTGACGCTCCCTGCTCTGAACACGCGCGCTGCTTGTATTTCACAAAGAT 1250
Qy 354 -CysAsnAlaAspAlaTyrGlnGlyGluValThrGluLysMetMetCysAlaGlyIle 373
Db 1251 CTGCAACACACAGGACGCTGACGGTGGCATCATCTCCCTCCATGCTCTCGCGGGGCTA 1310
Qy 373 eProGluGlyGlyValAspThr---CysGlnGlyAspSerGlyGlyProLeuMetTyrGln 392
Db 1311 CCTGACGGTGGCTTGGAAACAGCTGCCAGGGGACACGCGGGGGCCCTGGTGTGTCAA 1370
Qy 393 SerAspGln---TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGlyPro 411
Db 1371 GAGAGGAGGCTGTGAAAGTTAGTGGAGCGACCGAGCTTTGGCATCGGCTGCGCAGAGCTG 1430
Qy 412 SerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyrAsnValTrp 431
Db 1431 AACAGCTGGGTGTACACCGGTGTCCTCTCTGACTGGATCCACGACAGATG 1490
Qy 432 LysAlaGluLeu 435
Db 1491 GAGAGACCTA 1502

```


Alignment Scores:
Pred. No.: 1,36e-53 Length: 1783
Score: 584.50 Matches: 140
Percent Similarity: 45.05% Conservative: 60
Best Local Similarity: 31.53% Mismatches: 161
Query Match: 24.96% Indels: 83
DB: 4 Gaps: 11

US-09-607-745-2 (1-435) x US-09-861-966-188 (1-1783)

QY 19 LysProArgIleProMetGluThrPheArgLysValGlyLeuProIleIleAlaLeu 38
Db AGACCCAGGTGGCAGCTCTCACT-----GCCGGGACCTGCTACTTCTGACAGCC 338
QY 39 LeuSerLeuAlaSerIleIleValValValLeuLeuLysValIleLeuAspLysTyr 58
Db ATCGGGCGGCATCCTGGCGCATTTGGCTTCTCTCCTCAGG----- 380
QY 59 TyrPheLeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGlu 78
Db 380 ----- 380
QY 79 LeuAspCysProLeuGlyGluAspGluHisCysValLysSerPheProGluGlyPro 98
Db 381 -----AGTGACGAGG-----CCG 395
QY 99 AlaValAlaValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThr 118
Db CTGTACCCAGTCAGGTGAGTCTCGCGGAGCTCGGCTCATGTGTTTGTGACAAAGCGAA 455
QY 119 GlyAsnTrpPheSerAlaCysPheAspAsnPhetrGluAlaLeuAlaGluThrAlaCys 138
Db 456 GGGAGCTGGGGCTGCTGCTCTCGGCTCCAAACCGCGGGTAGCGGACTCAGCTGC 515
QY 139 ArgGlnMetGlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGln 158
Db 516 GAGGAGATGGCTTC-----CTCAGGCACTG-----ACCCACTCC 551
QY 159 AspLeuAspValValGluIleThrGluAsn----- 168
Db 552 GAGCTGACGTGCGAACCGGGCGCGCAATGGCAGCTCGGCTTCTTCTGTGGAGCAG 611
QY 169 -----SerGlnGluArgMetArgAsnSerSerGlyProCysLeuSer 183
Db 612 GGGAGGTGCCCCACACCCAGAGCTGCTGGAGTCACTCCGTGTGTGATGCCCCAGA 671
QY 184 GlySerLeuValSerLeuHisCysLeuAlaCysGly---LysSerLeuLysThrProArg 202
Db 672 GGGCGTCTTGTGGCGCCCATCTGCCAAGACTGTGGCGCAGAGCTGCCCGTGACCGC 731
QY 203 ValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGlnTyr 222
Db 732 ATCTGGAGCGGGACACAGCTGTGGCGCGTGGCGCGTGGCGAAGTCAGCTCGGTAT 791
QY 223 AspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAlaAla 242
Db 792 GATGAGCACACCTCTGTGGGGATCCCTGCTCTCGGGGACTGGTGTCTGACACCGCC 851
QY 243 HisCysPheArgLysHisThrAspValPheAsn---TrpLysValArgAlaGlySerAsp 261
Db 852 CACTGCTTCCCGAGCGAACCGGCTCTGTCCCGATGGCGAGTGTGTGGCGTGGCGGTG 911
QY 262 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 281
Db 912 GCCCAGGCTCTCCCCAGCTGTGACGTGGGGGTGAGCGTGGTGTACCCAGGGGGC 971
QY 282 MetTyrPro-----LysAspAsnAspIleAlaLeuMetLys 293
Db 972 TATCTTCTTTCGGGACCCCAACAGCGAGGAGACACACGATATGCTGCTGCTCCAC 1031
QY 294 LeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhePheAsp 313

QY 314 GluGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsn 333
Db 1092 CAGGCCCTGTGTGGTGGCAAGATCTGTACCTGACGGCTGGGGCAACACG---CAGTAC 1148
QY 334 GlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSerThrArg 353
Db 1149 TATGCCCAACAGCGCGGGTACTCAGGAGGCTCGAGTCCCATATCAGCAATGATGTC 1208
QY 354 CysAsnAlaAspAlaThrGlnGlyGluValThrGluLysMetMetCysAlaGlyIle 373
Db 1209 TGCATGGCGTGAATCTTATGGAACACAGATCAAGCCCAAGATGTTCTGTCTGGCTAC 1268
QY 374 ProGluGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGln--- 392
Db 1269 CCGAGGGTGGCATTCATCCCTGCCAGGGCGACAGCGTGTGCTCTTGTGTGAGGAC 1328
QY 393 -----SerAspGlnTrpHisValValGlyIleValSerTrpGlyTyrGlyCys 408
Db 1329 ASCATCTCTCGACCCAGCTTGGCGCTGTGGCATTTGAGTTGGGCACTGGCTGT 1388
QY 409 GlyGlyProSerThrProGlyValThrLysValSerAlaTyrLeuAsnTrpIleTyr 428
Db 1389 GCCTGGCCAGACAGCGGCTCTACACCAAGTCAGTCACTCCGGGAGTGGATCTTC 1448
QY 429 AsnValTrpLys 432
Db 1449 CAGGCCATAAAG 1460

RESULT 12
US-09-742-703-3
Sequence 3, Application US/09742703
Patent No. 6423543
GENERAL INFORMATION:
APPLICANT: Patrick Allen Marcotte
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTIGENSE MODULATION OF HEPSEN EXPRESSION
FILE REFERENCE: RTS-0090
CURRENT APPLICATION NUMBER: US/09/742,703
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 3
LENGTH: 2363
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (826)..(2079)
US-09-742-703-3

Alignment Scores:
Pred. No.: 2,11e-53 Length: 2363
Score: 584.50 Matches: 140
Percent Similarity: 45.05% Conservative: 60
Best Local Similarity: 31.53% Mismatches: 161
Query Match: 24.96% Indels: 83
DB: 4 Gaps: 11

US-09-607-745-2 (1-435) x US-09-742-703-3 (1-2363)

QY 19 LysProArgIleProMetGluThrPheArgLysValGlyLeuProIleIleAlaLeu 38
Db 868 AGACCCAGGTGGCAGCTCTCACT-----GCCGGGACCTGCTACTTCTGACAGCC 918
QY 39 LeuSerLeuAlaSerIleIleValValValLeuLeuLysValIleLeuAspLysTyr 58
Db 919 ATCGGGCGGCATCCTGGGCGCATTTGGCTTCTCTCCTCAGG----- 960
QY 59 TyrPheLeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGlu 78
Db 960 ----- 960

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QY 79 LeuAspCysProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyPro 98
Db 961 -----AGTACCAGGAG-----CCG 975
QY 99 AlaValAlaValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThr 118
Db 976 CTGTACCCAGTGCAGCTCAGCTCTCGGAGCTCCAGCTCCAGCCAGGAGTCCAGTCTTTGACAGACGGAA 1035
QY 119 GlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCys 138
Db 1036 GGGAGCTGGCGCTCTGTCTCTCGCTCCAGCTCCAGCCAGGAGTCCAGTCTTTGACAGACGGAA 1095
QY 139 ArgGlnMetGlyTyrSerSerLysProThrPheArgAlaValGluLeuGlyProAspGln 158
Db 1036 GAGGAGATGGGCTTC-----CTCAGGGCACTG-----ACCCACTCC 1131
QY 159 AspLeuAspValValGluLeuThrGluAsn-----168
Db 1132 GAGCTGGAGCTCCGAAAGCGGGCGGCAATGGCAGCTCGGGCTTCTTGTGTGGACAGAG 1191
QY 169 -----SerGlnGluLeuArgMetArgAsnSerSerGlyProCysLeuSer 183
Db 1192 GGGAGCTGCCACACACAGAGCTGCTGGAGGTATCTCCGTGTGTGATTGCCCCAGA 1251
QY 184 GlySerLeuValSerLeuHisCysLeuAlaCysGly---LysSerLeuLysThrProArg 202
Db 1252 GCGCGTTCTTGGCGGCTCTGCCAAGACTGTGGCGGAGGAGTCCCGTGGACCGC 1311
QY 203 ValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGlnTyr 222
Db 1312 ATCGTGGAGCGGGACACAGCTGTGGCGGCTGGCGGTGGCAAGTCAAGCTTTCGTAT 1371
QY 223 AspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAlaAla 242
Db 1372 GATGGAGCACACTCTGTGGGATCCCTGCTCTCGGGGACTGGGTGTGACAGCGGC 1431
QY 243 HisCysPheArgLysHisThrAspValPheAsn---TrpLysValArgLagLysAsp 261
Db 1432 CACTGCTTCCCGAGCGGAACCGGCTCTTCCGATGGCGAGTGTTCGCGGTGCGGTG 1491
QY 262 LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsnPro 281
Db 1492 GCGCAGGCTCTCCACAGCTGTGACGTGGGGTGCAGGTGTGTGTACACAGGGGGC 1551
QY 282 MetTyrPro-----LysAspAsnAspIleAlaLeuMetLys 293
Db 1552 TATCTTCCCTTTCGGACCCCAACAGCAGGAGAACAGCAAGATATTGCCCTGTGCCAC 1611
QY 294 LeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhePheAsp 313
Db 1612 CTCTCCAGTCCCTGCCCTCAGAGATACATCCAGCTGTGTGTCCAGTCCCGGC 1671
QY 314 GluGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsn 333
Db 1672 CAGGCTGTGTGATGGCAAGTCTCTACCGTACCGGGTGGGGCAACAG---CAGTAC 1728
QY 334 GlyGlyLysMetSerAspIleLeuGlnAlaSerValGlnValIleAspSerThrArg 353
Db 1729 TATGGCAACAGCGGGGTACTCCAGGAGGTTCGAGTCCCAATATCCAGTATGATGTC 1788
QY 354 CysAsnAlaAspAlaValGlnGlyGluValThrGluLysMetMetCysAlaGlyIle 373
Db 1789 TGAATGGCGCTCACTTCTATGGAACACAGATCAAGCCCAAGATGTTCTGTGTGCTAC 1848
QY 374 ProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGln---392
Db 1849 CCGAGGGTGCATTGATCTCCAGGGGACAGCGGTGTCTCTTGTGTGTGAGGAC 1908
QY 393 -----SerAspGlnTrpHisValValGlyIleValSerTrpGlyTyrGlyCys 408
Db 1909 AGCATCTCGGACGCGCAGTTCGGCGCTGTGTGGCATTGTGATTTGGGCACTGGCTGT 1968
QY 409 GlyGlyProSerThrProGlyValTyrThrLysValSerAlaTyrLeuAsnTrpIleTyr 428
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Db 1969 GCCCTGGCCAGAACCCAGGCGTCTACACCAAGTCACTGCTCCGGGAGTGGATCTTC 2028
QY 429 AsnValTrpLys 432
Db 2029 CAGGCCATAAAG 2040
RESULT 13
US-09-820-002-1
; Sequence 1, Application US/09820002
; Patent No. 6482630
; GENERAL INFORMATION:
; APPLICANT: Gan, Weinlu
; APPLICANT: Ye, Jane
; APPLICANT: DiFrancesco, Valentina
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001194
; CURRENT APPLICATION NUMBER: US/09/820,002
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1615
; TYPE: DNA
; ORGANISM: HUMAN
US-09-820-002-1
Alignment Scores:
Score: 3.6e-53 Length: 1615
Percent Similarity: 580.00 Matches: 132
Best Local Similarity: 44.06% Conservative: 57
Query Match: 30.77% Mismatches: 146
Indels: 94
Gaps: 9
US-09-607-745-2 (1-435) x US-09-820-002-1 (1-1615)
QY 19 LysProArgIleProMetGluThrPheArgLysValGlyIleProIleIleIleAlaLeu 38
Db 220 AGACCAAGTGGCGAGCTCTCACT-----GCGGGACCCCTGCTACTTCTGACAGCC 270
QY 39 LeuSerLeuAlaSerIleIleIleValValValLeuIleLysValIleLeuAspLysTyr 58
Db 271 ATCGGGCGGCATCTCGGCGCATTTGTGCTGTCTCTCTCAGG-----312
QY 59 TyrPheLeuCysGlyGlnProLeuHisPheIleProArgLysGlnLeuCysAspGlyGlu 78
Db 312 -----312
QY 79 LeuAspCysProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyPro 98
Db 313 -----AGTGACAGGAG-----CCG 327
QY 99 AlaValAlaValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThr 118
Db 328 CTGTACCCAGTGCAGCTCAGCTCTCGGAGCTCGGCTCATGCTCTTTGACAGACGGAA 387
QY 119 GlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCys 138
Db 388 GGGAGCTGGCGGTCTGTCTCTCGCTCCAAACGCGGAGTACCGGACTCAGCTGC 447
QY 139 ArgGlnMetGlyTyrSerSerLysProThrPheArgAlaValGluLeuGlyProAspGln 158
Db 448 GAGGAGATGGGCTTCTCAGT-----468
QY 159 AspLeuAspValValGluLeuThrGluAsnSerGlnGluLeuArgMetArgAsnSerSer 178
Db 468 -----468
QY 179 GlyProCysLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGly---LysSer 197
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Db 469 ---GATTGCCAGAGCGCGTTCTTGCGCGCCATCTGCCAAGACTGTGCGCGCAGGAAG 525
QY 198 LeuLysThrProArgValValGlyGlyGluGluAlaSerValAlaSerTrpProTrpGln 217
Db 526 CTCGCCGTGACCGCATCTGCGGAGGCGCGGACACACAGCTTGGCGCGGTGCGCGTGC 585
QY 218 ValSerIleGlnTrpAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrp 237
Db 586 GTACAGCTTGCTATGATGAGACACACTCTGTGGGATCCCTGCTCTCCGGGACTGG 645
QY 238 ValLeuThrAlaAlaHisCysPheArgLysHisThrAspValPheAsn---TrpLysVal 256
Db 646 GTGCTGACGCGCCACTCTCCCGAGGCGGAACCGGTCCTGTCCTCCGATGCGAGTG 705
QY 257 ArgAlaGlySerAspLysLeuGlySerPheProSerLeuAlaValAlaLysIleIle 276
Db 706 TTTGCCGTGCGCGGCGGCGCCACTCTCCACAGCTCTGCAGCTGGGGGTGCAGGCTGTG 765
QY 277 IleGluPheAsnProMetTyrPro-----LysAspAsnAsp 288
Db 766 GTCTACACGCGGGCTATCTTCCTTTCGGGACCCCAACGAGGAGAGACAGACAGAT 825
QY 289 IleAlaLeuMetLysLeuGlnPheProLeuThrPheSerGlyThrValArgProIleCys 308
Db 826 ATTGCCCTGTCTCCACTCTCCAGTCCCTGCTCCCTCACAGATATACACAGCTGTGTC 885
QY 309 LeuProPhePheAspGluGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGly 328
Db 886 CTCCTGCTGCGCGCGGCGGCTCTGCTGATGCGGAGTCTGTACCGGTGCGGCGTGGGC 945
QY 329 PheThrLysGlnAsnGlyGlyLysMetSerAspIleLeuGlnAlaSerValGlnVal 348
Db 946 AACACG---CAGTACTATGCGCACAGCGCGGCTACTCCAGAGGCTCGAGTCCCAT 1002
QY 349 IleAspSerThrArgCysAsnAlaAspAlaTyrGlnGlyGluValThrGluLysMet 368
Db 1003 ATCAGCAATGATGTCTCAATGGCGTGACTCTTATGGAACACAGATCAAGCCCAAGATG 1062
QY 369 MetCysAlaGlyIleProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyPro 388
Db 1063 TTTCTGTCTGCTACTCCCGCGGCTGCTGATGCTGCGGCGGCGAGCGGCTGCTCC 1122
QY 389 LeuMetTyrGln-----SerAspGlnTrpHisValValGlyIleValSer 403
Db 1123 TTTGTGTGTGAGGACAGCATCTCTCGACGCGCATGTTGGCGGCTGTGGCATTTGAGT 1182
QY 404 TrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSerAlaTyr 423
Db 1183 TGGGGCACTGCTGTGCTGCGGCGGCGGAGCGGCTGTACACCAAGTCAGTGACTTC 1242
QY 424 LeuAsnTrpIleTyrAsnValTrpLys 432
Db 1243 CGGAGTGGATCTTCCAGGCGCATAAAG 1269

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RESULT 14

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US-09-000-846-1
; Sequence 1, Application US/09000846
; Patent No. 5981830
; GENERAL INFORMATION:
; APPLICANT: WU, QINGYU
; APPLICANT: SADLER, JASPER
; TITLE OF INVENTION: KNOCKOUT MICE AND THEIR PROGENY WITH
; TITLE OF INVENTION: DISRUPTED SERINE PROTEASE GENES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: MILLER, WHITE, ZELANO & BRANTIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/000,846
; FILING DATE: 30-DEC-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/866,058
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: LEBOVITZ, RICHARD M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: BERLX 65P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1605 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 35..1282
; US-09-000-846-1

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Alignment Scores:

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Pred. No.: 5.88e-53 Length: 1605
Score: 578.00 Matches: 136
Percent Similarity: 47.43% Conservative: 58
Best Local Similarity: 33.25% Mismatches: 152
Query Match: 2 Indels: 63
DB: 11 Gaps: 11

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US-09-607-745-2 (1-435) x US-09-000-846-1 (1-1605)

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QY 62 CysGlyClnProLeuHisPheIleProArgLysGln-----LeuCysAspGlyGluLeu 79
Db 97 TGTGGGTACCTCTCT-----GTCTCTGACAGCATTTGGGCGCGCTCTGGGCGCATTTGT 150
QY 80 AspCysProLeuGlyGlu-AspGluGluHisCysValLysSerPheProGluGlyProAl 99
Db 151 GACATCTCTACTGCAGAGTACCAGGAG-----CCACT 183
QY 99 aValAlaValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGl 119
Db 184 GTACCAAGTGCAGTCCAGTCCAGGAGACTCACGGCTTGGCTTTTTCACAAAGACGGAGGG 243
QY 119 yAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysAr 139
Db 244 AACGTGGAGGCTACTGTGCTCTCTCACGCTCCAATGCCAGGCTGCGGCTCGGCTGTGA 303
QY 139 gGlnMetGlyTyr----- 143
Db 304 GGAGATGGGCTTTCTCAGGCGCTCTGGCGGACTCGGAGCTGGATGTCGGACTCGGGCGC 363
QY 144 -SerSerLysProThrPheArgAlaValGluIleGly-----ProAspGlnAs 159
Db 364 CAACGGCAGCATCGGCTCTTTTTCGTGGACGAGGCGGAGCTCCGCTCGCTCAGAGTT 423
QY 159 pLeuAspValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGl 179
Db 424 GCTGGATGTCATCTCTGTATGAC----- 448
QY 179 yProCysLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGly---LysSerLe 198

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Db 449 ----TGTCCTAGAGCCGACATTCCTGACTGCCACCTGCCAAGACTGTGGCCGAGGAGCT 504
Qy 198 ulysThrProArgValValGlyGluGluAlaSerValAspSerTrpProTrpGlnVa 218
Db 505 GCCGTGTGACCGCATGTGGGGGGGCGAGACAGCAGTCTGGGAAGGTGGCCGTCGACG 564
Qy 218 lserIleGlnTrpAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpVa 238
Db 565 CAGCCTGGCTGTATGATGGGACCCACTCTGTGTGGGGGTCCCTGTCTGTGGGGATGGGT 624
Qy 238 lleuThrAlaAlaHisCysPheArgLysHisThrAspValPheAsn---TrpLysValar 257
Db 625 GCTGACTCTGCACATTCCTTTCCAGCGGGAACCGGGTCTCTGTCGTGGCGAGTATT 684
Qy 257 gAlaGlySerAspLysLeuGlySerPheProSerLeuAlaValAlaLysIleIleI 277
Db 685 TGCTGTGCTGTAGCCCGGACCTCACCATCTCTGTGCACTGGGGTTCAGGCTGTGAT 744
Qy 277 eGluPheAsnProMetTrpPro-----LysAspAsnAspI 289
Db 745 CTATCATGGGGCTACCTTCCTTCCTTCGAGACCTACTATCGACGAAACAGCAATGACAT 804
Qy 289 eAlaLeuMetLysLeuGlnPheProLeuThrPheSerGlyThrValArgProIleCysI 309
Db 805 TCCTGTGTGTCACCTCTCTAGTCCCTCTCCTCACAGAATACATCCACCGCAGTGTCT 864
Qy 309 uProPhePheAspGluGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPh 329
Db 865 CCTGCTGGGACAGCCCTGTGTGATGGCGCAGGTCTCTACTGTGACCGCTGGGGTAA 924
Qy 329 eThrLysGlnAsnGlyGlyLysMetSerAspIleLeuLeuGlnAlaSerValGlnVal 349
Db 925 CACA---CAGTTCTATGGCCACAGCTATGCTGCCAAGAGGCGCGGTTCCTCATCAT 981
Qy 349 eAspSerThrArgCysAsnAlaAspAlaTyrglnGlnGluValThrGluLysMetMe 369
Db 982 AAGCAACGAAGTTTGCAACAGCCCGACTTTCACGGGAATCAGATCAAGCCCAAGATGT 1041
Qy 369 tCysAlaGlyIleProGluGlyValAspThrCysGlnGlyAspSerGlyGlyProle 389
Db 1042 CTGTCTGGCTATCTCTAGGGTGGATGTATGCTGCCAGGGCGACAGTGGAGGCCCTT 1101
Qy 389 uMetTrpGln-----SerAspGlnTrpHisValValGlyIleValSerTr 404
Db 1102 TGTGTGTGAAGACAGCATCTCTGGGACATCAAGTGGGGCTATGTGGCATTTGTAAGCTG 1161
Qy 404 pGlyTrpGlyCysGlyGlyProSerThrProGlyValTyThrLysValSerAlaTyrl 424
Db 1162 GGGTACGGGCTGTCTTTGGCCCGGAAGCCAGGAGTGTACACAAAGTCACTGACTTCG 1221
Qy 424 uAsnTrpIleTyAsnValTrpLys 432
Db 1222 GGAGTGGATCTTCAAGGCCATTAAG 1246
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RESULT 15

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US-09-370-838-80
; Sequence 80, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; EARLY STAGE OF LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 80
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-370-838-80
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Alignment Scores:

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Pred. No.: 8.37e-53 Length: 1460
Score: 576.00 Matches: 145
Percent Similarity: 50.88% Conservative: 86
Best Local Similarity: 31.94% Mismatches: 161
Query Match: 24.59% Indels: 62
DB: 4 Gaps: 16
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US-09-607-745-2 (1-435) x US-09-370-838-80 (1-1460)

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Qy 5 SerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArgIleProMet 24
Db 19 GCAGAAAAAGAACCTCTTCATTAAAGATTAAAAATGATAGCCGACGACGTGTA---ACT 75
Qy 25 GluThrPheArgLysValGlyIleProIleIleIleAlaLeuSerLeuAlaSerIle 44
Db 76 TCGACTTCAAGATTCTGAAT---CCATATGATGATGTTTCATTCGTGCGAGGGTA 132
Qy 45 IleIleValValValIleLysValIleLeuAspLysTyTrpPheLeuCysGlyGln 64
Db 133 GTGATCTCGGCGATCACCATAGCTCTACTTGT---TACTTTTACTCTTTGAT 183
Qy 65 ProLeuHisPheIleProArgLys-----GlnLeuCysAspGlyGluLeuAspCysPro 82
Db 184 CAAAAATCTTACTTTTATAGGAGCAGTTTCACTCTCAATATGTTGAATATAATAGTCAG 243
Qy 83 Leu-----GlyGluAspGluGluHisCys 90
Db 244 TTAATTCACCGCTACACAGGATACAGACTTTGATGGAGAAATGAATCTCTGATT 303
Qy 91 ValLysSerPheProGluGly-----ProAlaValAlaValArg 103
Db 304 ACTAAACATTCAAAGAATCAATTTAAGAAATCAGTTTCATCAGAGCTCATGTTGCCAA 363
Qy 104 LeuSerLysAsp-----ArgSerThrLeuGlnValLeuAspSerAlaThrGly 119
Db 364 CTGAGGCAAGATGTGTAGTGTGTGAGAGCGGATGTTGTCATGAAATTTCAATTCCTAGA 423
Qy 120 AsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArg 139
Db 424 AATAACATGAGGATCAATG-----AAAGCAGAAATGAGTCTGTTTACGA 471
Qy 140 GlnMetGlyTyTrpSerLysProThrPheArgAlaValGluIleGlyProAspGlnAsp 159
Db 472 CAATGCTGAATAACTCT-----GGAACCTGGAATAAACCCT---TCA 513
Qy 160 LeuAspValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsn-----Ser 177
Db 514 ACTGAGATAACATCATTACTGACCGGCTCGACAAATTCGCTATTATTAATGAATGCGG 573
Qy 178 SerGlyProCysLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSer 197
Db 574 GCCGCTCCAGACTAATA-----GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 594
Qy 198 LeuLysThrProArgValValGlyGlyGluAlaSerValAspSerTrpProTrpGln 217
Db 595 TTGTCTGAGCAGAGATCTCTTGGAGGCACTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAG 654
Qy 218 ValSerIleGlnTrpAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrp 237
Db 655 GTGAGTCTGGGCTCAATAATGCCCCACCTGTCGAGGAGGAGGAGGAGGAGGAGGAGGAG 714
Qy 238 ValLeuThrAlaAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArg 257
Db 715 ATCTTGACAGCAGTCTACTGCTTCAGAGCACTCTAATCTCTGCTGAGTGGATGCCAGC 774
Qy 258 AlaGlySerAspLysLeuGlySerPheProSerLeu-----AlaValAlaLysIle 275
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Db 775 TCTGGTATTTCACAC-----ACATTTCCTAACTAAGATGAGAGTAAGAAATATTTTA 828
QY 276 IleIleGluPheAsnProMetTyProLysAspAsnAspIleAlaLeuMetLysLeuGln 295
Db 829 ATTCATAACAAATTATAAATCTGCAACTCATGAAATGACATTGCATTGTGAGACTTGAG 888
QY 296 PheProLeuThrPheSerGlyThrValArgProIleCysLeuProPhePheAspGluGlu 315
Db 889 AACAGTGTACCTTTACAAAGATATCCATAGTGTGTCTCCAGCTGTACCCAGAAT 948
QY 316 LeuThrProAlaThrProLeuThrIleIleGlyTyrGlyPheThrLysGlnAsnGlyGly 335
Db 949 ATTCACCTTGGCTCTACTGCTTATGTACAGGATGGGGGCTCAAGATATGTCTGGCCAC 1008
QY 336 LysMetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsn 355
Db 1009 ACAGTTCACAGAG--CTAAGGCAAGGACAGCTCAGAATAATAAGTAATGATGTATGTAAT 1065
QY 356 AlaAspAspAlaTyrgInGlyGluValThrCluLysMetMetCysAlaGlyIleProGlu 375
Db 1066 GCACCAATAGTTATATAGGAGCCATCTGTCTGGAATGCTGTGTCTGGAGTACCTCAA 1125
QY 376 GlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrgInSerAspGln 395
Db 1126 GGTGGAGTGGACGCGCATGTCAGGGTGACTCTGTGTGGCCCACTAGTACAAGAAGACTCACGG 1185
QY 396 -----TrpHisValValGlyIleValSerTrpGlyTyrgLysGlyGlyProSerThr 413
Db 1186 CGGCTTTGGTTTATGTGGGATAGTAAGCTGGGGAGATCAGTGTGGCCTGCCGGATAAG 1245
QY 414 ProGlyValTyrrLysValSerAlaTyrrLeuAsnTrpIle 427
Db 1246 CCAGGAGTGTATCTCGAGTGACAGCCPACCTTGACTGGATT 1287
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Search completed: December 2, 2003, 02:54:14
Job time : 107.769 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 02:15:49 ; Search time 324.904 Seconds
(without alignments)
246.943 Million cell updates/sec

Title: US-09-607-745-2

Perfect score: 2342

Sequence: 1 MDPDSQPLNSLDVKPLRKP.....VYTKVSAYLNWYNWKAEL 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2338	99.8	435	12	US-10-180-719-6
2	2337	99.8	437	9	US-09-851-588-8
3	2319	99.0	437	11	US-09-776-191-4
4	2297.5	98.1	432	11	US-09-888-257A-7
5	2297.5	98.1	432	11	US-09-946-374-275
6	2297.5	98.1	432	12	US-10-015-387A-275
7	2297.5	98.1	432	12	US-10-063-735-112
8	2297.5	98.1	432	12	US-10-006-130A-275
9	2297.5	98.1	432	12	US-10-199-672-330
10	2297.5	98.1	432	12	US-10-006-172A-275
11	2297.5	98.1	432	12	US-10-187-749-330
12	2297.5	98.1	432	12	US-10-184-457-330
13	2297.5	98.1	432	12	US-10-184-642-330
14	2297.5	98.1	432	12	US-10-196-747-330
15	2297.5	98.1	432	12	US-10-015-392A-275

16 2297.5 98.1 432 12 US-10-017-253A-275
17 2297.5 98.1 432 12 US-10-173-689-330
18 2297.5 98.1 432 12 US-10-173-690-330
19 2297.5 98.1 432 12 US-10-173-691-330
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29 2297.5 98.1 432 12 US-10-174-591-330
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32 2297.5 98.1 432 12 US-10-175-744-330
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38 2297.5 98.1 432 12 US-10-176-489-330
39 2297.5 98.1 432 12 US-10-176-754-330
40 2297.5 98.1 432 12 US-10-176-755-330
41 2297.5 98.1 432 12 US-10-176-759-330
42 2297.5 98.1 432 12 US-10-176-920-330
43 2297.5 98.1 432 12 US-10-176-922-330
44 2297.5 98.1 432 12 US-10-176-924-330
45 2297.5 98.1 432 12 US-10-176-984-330

ALIGNMENTS

RESULT 1
US-10-180-719-6
; Sequence 6, Application US/10180719
; Publication No. US20030166246A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/180,719
; FILING DATE: 25-Jun-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271
; FILING DATE: 16-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555

```
TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 435 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: COLNNOT13
;   CLONE: 1337018
; SEQUENCE DESCRIPTION: SEQ ID NO: 6 :
US-10-180-719-6

Query Match          99.8%; Score 2338; DB 12; Length 435;
Best Local Similarity 99.8%; Pred. No. 5.3e-226;
Matches 434; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPDSDQPLNSLDVKKPLRPKPRIPMETFRKVGIPIIIIALLSLASIIIVVLIKILDKYIF 60
DB 1 MPDSDQPLNSLDVKKPLRPKPRIPMETFRKVGIPIIIIALLSLASIIIVVLIKILDKYIF 60
QY 61 LCGQPLHFIPRKQDCGELDCPLGEDEEHCVKSPFEGPAVAVRLSKDRSTLQVLDSATGN 120
DB 61 LCGQPLHFIPRKQDCGELDCPLGEDEEHCVKSPFEGPAVAVRLSKDRSTLQVLDSATGN 120
QY 121 WFSACFDNTEALAEATACRQMGYSKPTFRVAVIGDPDQLDVVEITENSQELMRNSSGP 180
DB 121 WFSACFDNTEALAEATACRQMGYSKPTFRVAVIGDPDQLDVVEITENSQELMRNSSGP 180
QY 181 CLSGSLVSLHCLACGSLKTPRVVGGEASVDSWPQVSIQYDKQHVCGSILDPHWLTA 240
DB 181 CLSGSLVSLHCLACGSLKTPRVVGGEASVDSWPQVSIQYDKQHVCGSILDPHWLTA 240
QY 241 AAHCFRKHTDVFNWKVRAGSDKLGSPFLAVAKIIIEFNPMYPKNDIALMKLQPLTF 300
DB 241 AAHCFRKHTDVFNWKVRAGSDKLGSPFLAVAKIIIEFNPMYPKNDIALMKLQPLTF 300
QY 301 SGTVRPICLPFFDEELTPATPLMIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDA 360
DB 301 SGTVRPICLPFFDEELTPATPLMIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDA 360
QY 361 QGEVTEKMCAGIPREGVDTCCGDSGGLMYQSDQHVHVGVISWGYCGGSPTPGVYTKV 420
DB 361 QGEVTEKMCAGIPREGVDTCCGDSGGLMYQSDQHVHVGVISWGYCGGSPTPGVYTKV 420
QY 421 SAYLNWIYNVWKAEL 435
DB 421 SAYLNWIYNVWKAEL 435

RESULT 2
US-09-851-588-8
; Sequence 8, Application US/09851588
; Patent No. US20020042067A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt C.
; APPLICANT: Wilson, Keith E.
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, AND COMPOSITIONS, AND
; FILE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; TITLE REFERENCE: A-68829-1/DJB/JJD/AMS
; CURRENT APPLICATION NUMBER: US/09/851,588
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/642,252
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: US 09/656,002
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match          99.0%; Score 2319; DB 11; Length 437;
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US-09-851-588-8

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Query Match          99.8%; Score 2337; DB 9; Length 437;
Best Local Similarity 100.0%; Pred. No. 6.7e-226;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DPDSQPLNSLDVKKPLRPKPRIPMETFRKVGIPIIIIALLSLASIIIVVLIKILDKYIF 61
DB 4 DPDSQPLNSLDVKKPLRPKPRIPMETFRKVGIPIIIIALLSLASIIIVVLIKILDKYIF 63
QY 62 CQOPLHFIPRKQDCGELDCPLGEDEEHCVKSPFEGPAVAVRLSKDRSTLQVLDSATGN 121
DB 64 CQOPLHFIPRKQDCGELDCPLGEDEEHCVKSPFEGPAVAVRLSKDRSTLQVLDSATGN 123
QY 122 FSACFDNTEALAEATACRQMGYSKPTFRVAVIGDPDQLDVVEITENSQELMRNSSGP 181
DB 124 FSACFDNTEALAEATACRQMGYSKPTFRVAVIGDPDQLDVVEITENSQELMRNSSGP 183
QY 182 LSGSLVSLHCLACGSLKTPRVVGGEASVDSWPQVSIQYDKQHVCGSILDPHWLTA 241
DB 184 LSGSLVSLHCLACGSLKTPRVVGGEASVDSWPQVSIQYDKQHVCGSILDPHWLTA 243
QY 242 AHCFRKHTDVFNWKVRAGSDKLGSPFLAVAKIIIEFNPMYPKNDIALMKLQPLTF 301
DB 244 AHCFRKHTDVFNWKVRAGSDKLGSPFLAVAKIIIEFNPMYPKNDIALMKLQPLTF 303
QY 302 GTVRPICLPFFDEELTPATPLMIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDA 361
DB 304 GTVRPICLPFFDEELTPATPLMIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDA 363
QY 362 GEVTEKMCAGIPREGVDTCCGDSGGLMYQSDQHVHVGVISWGYCGGSPTPGVYTKV 421
DB 364 GEVTEKMCAGIPREGVDTCCGDSGGLMYQSDQHVHVGVISWGYCGGSPTPGVYTKV 423
QY 422 AYLNIYNVWKAEL 435
DB 424 AYLNIYNVWKAEL 437
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RESULT 3

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US-09-776-191-4
; Sequence 4, Application US/09776191
; Publication No. US20030119168A1
; GENERAL INFORMATION:
; APPLICANT: Edwin L. Madison
; APPLICANT: Edgar O. Ong
; APPLICANT: Jiunn-Chern Yeh
; APPLICANT: Corvas International, Inc.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; FILE OF INVENTION: TRANSMEMBRANE SERINE PROTEASES, THE ENCODED PROTEINS AND
; TITLE REFERENCE: 24745-1607
; CURRENT APPLICATION NUMBER: US/09/776,191
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,124
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/234,840
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/179,982
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 60/183,542
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: 09/657,968
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-776-191-4
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Best Local Similarity 99.5%; Pred. No. 4.3e-224;
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 DPDSQPLNSLDVPLKPRIPMETFRKVGIPPIIIALLSLASIIIVVLIKVIDLKYFL 61
Db 4 DPDSQPLNSLDVPLKPRIPMETFRKVGIPPIIIALLSLASIIIVVLIKVIDLKYFL 63

QY 62 CGQPLHFIIPRKOLCDGELDCPLGEDEHCHVKSFPPEGPAVAVRLSKDRSTLQVLD SATGNW 121
Db 64 CGQPLHFIIPRKOLCDGELDCPLGEDEHCHVKSFPPEGPAVAVRLSKDRSTLQVLD SATGNW 123

QY 122 FSACFDNFTALAEATACRQMGYSKPTFRAVEIGPDQDLDVVEITENSQELMRNSSGPC 181
Db 124 FSACFDNFTALAEATACRQMGYSKPTFRAVEIGPDQDLDVVEITENSQELMRNSSGPC 183

QY 182 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPQVSIQYDKOHVCGGSLDPHWWLTA 241
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Db 244 AHCFRKHDFVFNWVVRAGSDKLGSPSLAVAKIIIEFNPMYPKNDIALMKLOPPLTFS 303

QY 302 GTVRPICLPFFDEELTPATPLWIIIGWFTKONGKMSDILLQASVQVIDSTRCNADDA YQ 361
Db 304 GTVRLICLPFFDEELTPATPLWIIIGWFTKONGKMSDILLQASVQVIDSTRCNADDA YQ 363

QY 362 GEVTEKMKCAGIPGEGVDTCQDSDGGLMYOSDQVHVVGI VSWGCGGPGSTPGVYTKVS 421
Db 364 GEVTEKMKCAGIPGEGVDTCQDSDGGLMYOSDQVHVVGI VSWGCGGPGSTPGVYTKVS 423

QY 422 AYLNIWYNNWKAEL 435
Db 424 AYLNIWYNNWKAEL 437

RESULT 4
US-09-888-257A-7
; Sequence 7, Application US/09888257A
; Publication No. US20030060612A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Polakis, Paul
; APPLICANT: Smith, Victoria
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5002R1
; CURRENT APPLICATION NUMBER: US/09/888,257A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/063,540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: US 60/089,653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/099,792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/103,678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: US 60/235,451
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 7
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-888-257A-7

Query Match 98.1%; Score 2297.5; DB 11; Length 432;
Best Local Similarity 98.8%; Pred. No. 6.1e-222;
Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 2 DPDSQPLNSLDVPLKPRIPMETFRKVGIPPIIIALLSLASIIIVVLIKVIDLKYFL 61
Db 4 DPDSQPLNSLDVPLKPRIPMETFRKVGIPPIIIALLSLASIIIVVLIKVIDLKYFL 63

QY 62 CGQPLHFIIPRKOLCDGELDCPLGEDEHCHVKSFPPEGPAVAVRLSKDRSTLQVLD SATGNW 121
Db 64 CGQPLHFIIPRKOLCDGELDCPLGEDEHCHVKSFPPEGPAVAVRLSKDRSTLQVLD SATGNW 123

QY 122 FSACFDNFTALAEATACRQMGYSKPTFRAVEIGPDQDLDVVEITENSQELMRNSSGPC 181
Db 124 FSACFDNFTALAEATACRQMGYSKPTFRAVEIGPDQDLDVVEITENSQELMRNSSGPC 178

QY 182 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPQVSIQYDKOHVCGGSLDPHWWLTA 241
Db 179 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPQVSIQYDKOHVCGGSLDPHWWLTA 238

QY 242 AHCFRKHDFVFNWVVRAGSDKLGSPSLAVAKIIIEFNPMYPKNDIALMKLOPPLTFS 301
Db 239 AHCFRKHDFVFNWVVRAGSDKLGSPSLAVAKIIIEFNPMYPKNDIALMKLOPPLTFS 298

QY 302 GTVRPICLPFFDEELTPATPLWIIIGWFTKONGKMSDILLQASVQVIDSTRCNADDA YQ 361
Db 299 GTVRPICLPFFDEELTPATPLWIIIGWFTKONGKMSDILLQASVQVIDSTRCNADDA YQ 358

QY 362 GEVTEKMKCAGIPGEGVDTCQDSDGGLMYOSDQVHVVGI VSWGCGGPGSTPGVYTKVS 421
Db 359 GEVTEKMKCAGIPGEGVDTCQDSDGGLMYOSDQVHVVGI VSWGCGGPGSTPGVYTKVS 418

QY 422 AYLNIWYNNWKAEL 435
Db 419 AYLNIWYNNWKAEL 432

RESULT 5
US-09-946-374-275
; Sequence 275, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830PIC1
CURRENT APPLICATION NUMBER: US/09/946,374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
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PRIOR APPLICATION NUMBER: 60/099815
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PRIOR FILING DATE: 1998-09-10
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PRIOR APPLICATION NUMBER: 60/101014
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101068
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PRIOR APPLICATION NUMBER: 60/101071
PRIOR FILING DATE: 1998-09-18
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PRIOR APPLICATION NUMBER: 60/102331
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102484
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PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102571
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102684
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103315
PRIOR FILING DATE: 1998-10-07

1 PRIOR APPLICATION NUMBER: 60/103328
2 PRIOR FILING DATE: 1998-10-07
3 PRIOR APPLICATION NUMBER: 60/103395
4 PRIOR FILING DATE: 1998-10-07
5 PRIOR APPLICATION NUMBER: 60/103396
6 PRIOR FILING DATE: 1998-10-07
7 PRIOR APPLICATION NUMBER: 60/103401
8 PRIOR FILING DATE: 1998-10-07
9 PRIOR APPLICATION NUMBER: 60/103449
10 PRIOR FILING DATE: 1998-10-06
11 PRIOR APPLICATION NUMBER: 60/103633
12 PRIOR FILING DATE: 1998-10-08
13 PRIOR APPLICATION NUMBER: 60/103678
14 PRIOR FILING DATE: 1998-10-08
15 PRIOR APPLICATION NUMBER: 60/103679
16 PRIOR FILING DATE: 1998-10-08
17 PRIOR APPLICATION NUMBER: 60/103711
18 PRIOR FILING DATE: 1998-10-08
19 PRIOR APPLICATION NUMBER: 60/104257
20 PRIOR FILING DATE: 1998-10-14
21 PRIOR APPLICATION NUMBER: 60/104987
22 PRIOR FILING DATE: 1998-10-20
23 PRIOR APPLICATION NUMBER: 60/105000
24 PRIOR FILING DATE: 1998-10-20
25 PRIOR APPLICATION NUMBER: 60/105002
26 PRIOR FILING DATE: 1998-10-20
27 PRIOR APPLICATION NUMBER: 60/105104
28 PRIOR FILING DATE: 1998-10-21
29 PRIOR APPLICATION NUMBER: 60/105169
30 PRIOR FILING DATE: 1998-10-22
31 PRIOR APPLICATION NUMBER: 60/105266
32 PRIOR FILING DATE: 1998-10-22
33 PRIOR APPLICATION NUMBER: 60/105693
34 PRIOR FILING DATE: 1998-10-26
35 PRIOR APPLICATION NUMBER: 60/105694
36 PRIOR FILING DATE: 1998-10-26
37 PRIOR APPLICATION NUMBER: 60/105807

Query Match 98.1%; Score 2297.5; DB 11; Length 432;
Best Local Similarity 98.8%; Pred. No. 6.1e-222;
Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
QY 2 DPDSQPLNSLDVPLKRPIMPETFRKVGIPITIIALLSLASIIIVVLIKVLIDKYFL 61
DB 4 DPDSQPLNSLDVPLKRPIMPETFRKVGIPITIIALLSLASIIIVVLIKVLIDKYFL 63
QY 62 CGQPLHFIIPRKQDCGELDCPLGEDEEHCHVKSPFPGPAVAVRLSKDRSTLQVLDSATGNW 121
DB 64 CGQPLHFIIPRKQDCGELDCPLGEDEEHCHVKSPFPGPAVAVRLSKDRSTLQVLDSATGNW 123
QY 122 FSACFDNFTALAEATACRMGYSSKPTFRAVEIGDPDQLDVVEITENSQELMRNSSGFC 181
DB 124 FSACFDNFTALAEATACRMGYSSKPTFRAVEIGDPDQLDVVEITENSQELMRNSSGFC 178
QY 182 LSGSLVSLHCLACGSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSIILDPHWLTA 241
DB 179 LSGSLVSLHCLACGSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSIILDPHWLTA 238
QY 182 LSGSLVSLHCLACGSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSIILDPHWLTA 241
DB 179 LSGSLVSLHCLACGSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSIILDPHWLTA 238
QY 242 AHCPRKHTDVFNWVKRAGSDKLGSPFLSAVAKIIIEFNPMYPKNDIALMKLOPLTFPS 301
DB 239 AHCPRKHTDVFNWVKRAGSDKLGSPFLSAVAKIIIEFNPMYPKNDIALMKLOPLTFPS 298
QY 302 GTVRPCLPFDEELTPATPLIIGWGTCKONGKMSDILLQASVOVIDSTRCNADDAVQ 361
DB 299 GTVRPCLPFDEELTPATPLIIGWGTCKONGKMSDILLQASVOVIDSTRCNADDAVQ 358
QY 362 GEVTEKMCAGIPEGGVDTCCQDSGGPLMYQSDQHVGVISWGWGCGGPGSTPGVYTKVS 421
DB 359 GEVTEKMCAGIPEGGVDTCCQDSGGPLMYQSDQHVGVISWGWGCGGPGSTPGVYTKVS 418
QY 422 AYLNWYINWVWKAEL 435
DB 419 AYLNWYINWVWKAEL 432

RESULT 7
US-10-063-735-112

RESULT 6

US-10-015-387A-275
; Sequence 275, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C34
; CURRENT APPLICATION NUMBER: US/10/015.387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 275
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-387A-275

Query Match 98.1%; Score 2297.5; DB 12; Length 432;
Best Local Similarity 98.8%; Pred. No. 6.1e-222;
Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
QY 2 DPDSQPLNSLDVPLKRPIMPETFRKVGIPITIIALLSLASIIIVVLIKVLIDKYFL 61
DB 4 DPDSQPLNSLDVPLKRPIMPETFRKVGIPITIIALLSLASIIIVVLIKVLIDKYFL 63
QY 62 CGQPLHFIIPRKQDCGELDCPLGEDEEHCHVKSPFPGPAVAVRLSKDRSTLQVLDSATGNW 121
DB 64 CGQPLHFIIPRKQDCGELDCPLGEDEEHCHVKSPFPGPAVAVRLSKDRSTLQVLDSATGNW 123
QY 122 FSACFDNFTALAEATACRMGYSSKPTFRAVEIGDPDQLDVVEITENSQELMRNSSGFC 181
DB 124 FSACFDNFTALAEATACRMGYSSKPTFRAVEIGDPDQLDVVEITENSQELMRNSSGFC 178
QY 182 LSGSLVSLHCLACGSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSIILDPHWLTA 241
DB 179 LSGSLVSLHCLACGSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSIILDPHWLTA 238
QY 242 AHCPRKHTDVFNWVKRAGSDKLGSPFLSAVAKIIIEFNPMYPKNDIALMKLOPLTFPS 301
DB 239 AHCPRKHTDVFNWVKRAGSDKLGSPFLSAVAKIIIEFNPMYPKNDIALMKLOPLTFPS 298
QY 302 GTVRPCLPFDEELTPATPLIIGWGTCKONGKMSDILLQASVOVIDSTRCNADDAVQ 361
DB 299 GTVRPCLPFDEELTPATPLIIGWGTCKONGKMSDILLQASVOVIDSTRCNADDAVQ 358
QY 362 GEVTEKMCAGIPEGGVDTCCQDSGGPLMYQSDQHVGVISWGWGCGGPGSTPGVYTKVS 421
DB 359 GEVTEKMCAGIPEGGVDTCCQDSGGPLMYQSDQHVGVISWGWGCGGPGSTPGVYTKVS 418
QY 422 AYLNWYINWVWKAEL 435
DB 419 AYLNWYINWVWKAEL 432

RESULT 7
US-10-063-735-112

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; Sequence 112, Application US/10063735
; Publication No. US20030138892A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,735
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 112
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-735-112

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Query Match      98.1%; Score 2297.5; DB 12; Length 432;
Best Local Similarity 98.8%; Pred. No. 6.1e-222;
Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 2 DPDSQPLNSLDVPLKRPRIPIETPRKVGIPITIIALLSLASIIIVVLLIKVILDKYFL 61
DB 4 DPDSQPLNSLDVPLKRPRIPIETPRKVGIPITIIALLSLASIIIVVLLIKVILDKYFL 63
QY 62 CQOPLHFIIPRKQDCGELDCPLGDEDEHCHVKSPFEGPFAVAVRLSKDRSTLOVLDSATGNW 121
DB 64 CQOPLHFIIPRKQDCGELDCPLGDEDEHCHVKSPFEGPFAVAVRLSKDRSTLOVLDSATGNW 123
QY 122 FSACDFNTEALAEACRONGYSKPTTFRAVEIGPDQDLVDVVEITENSQELMRNSSGFC 181
DB 124 FSACDFNTEALAEACRONGYS-----RAVEIGPDQDLVDVVEITENSQELMRNSSGFC 178
QY 182 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSIIDPHWLTA 241
DB 179 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSIIDPHWLTA 238
QY 242 AHCERKHTDVFNKVRAGSDKLGSPFSLAVAKIIIEFNPMYPKNDIALMKLQFLPTFS 301
DB 239 AHCERKHTDVFNKVRAGSDKLGSPFSLAVAKIIIEFNPMYPKNDIALMKLQFLPTFS 298
QY 302 GTVRPICLPFFDEELTPATPLMIIGWFTKONGKMSDILLQASVOVIDSTRCNADDAQ 361
DB 299 GTVRPICLPFFDEELTPATPLMIIGWFTKONGKMSDILLQASVOVIDSTRCNADDAQ 358
QY 362 GEVTERKMCAGIPEGGVDTCCQDSGGPLMYQSDQHWVGVISWGYCGGSPFPGVYTKVS 421
DB 359 GEVTERKMCAGIPEGGVDTCCQDSGGPLMYQSDQHWVGVISWGYCGGSPFPGVYTKVS 418
QY 422 AYLNWIYNNWKAEL 435
DB 419 AYLNWIYNNWKAEL 432

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RESULT 8
US-10-006-130A-275
; Sequence 275, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

```

```

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 275
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-130A-275

Query Match      98.1%; Score 2297.5; DB 12; Length 432;
Best Local Similarity 98.8%; Pred. No. 6.1e-222;
Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 2 DPDSQPLNSLDVPLKRPRIPIETPRKVGIPITIIALLSLASIIIVVLLIKVILDKYFL 61
DB 4 DPDSQPLNSLDVPLKRPRIPIETPRKVGIPITIIALLSLASIIIVVLLIKVILDKYFL 63
QY 62 CQOPLHFIIPRKQDCGELDCPLGDEDEHCHVKSPFEGPFAVAVRLSKDRSTLOVLDSATGNW 121
DB 64 CQOPLHFIIPRKQDCGELDCPLGDEDEHCHVKSPFEGPFAVAVRLSKDRSTLOVLDSATGNW 123
QY 122 FSACDFNTEALAEACRONGYSKPTTFRAVEIGPDQDLVDVVEITENSQELMRNSSGFC 181
DB 124 FSACDFNTEALAEACRONGYS-----RAVEIGPDQDLVDVVEITENSQELMRNSSGFC 178
QY 182 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSIIDPHWLTA 241
DB 179 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSIIDPHWLTA 238
QY 242 AHCERKHTDVFNKVRAGSDKLGSPFSLAVAKIIIEFNPMYPKNDIALMKLQFLPTFS 301
DB 239 AHCERKHTDVFNKVRAGSDKLGSPFSLAVAKIIIEFNPMYPKNDIALMKLQFLPTFS 298
QY 302 GTVRPICLPFFDEELTPATPLMIIGWFTKONGKMSDILLQASVOVIDSTRCNADDAQ 361
DB 299 GTVRPICLPFFDEELTPATPLMIIGWFTKONGKMSDILLQASVOVIDSTRCNADDAQ 358
QY 362 GEVTERKMCAGIPEGGVDTCCQDSGGPLMYQSDQHWVGVISWGYCGGSPFPGVYTKVS 421
DB 359 GEVTERKMCAGIPEGGVDTCCQDSGGPLMYQSDQHWVGVISWGYCGGSPFPGVYTKVS 418
QY 422 AYLNWIYNNWKAEL 435
DB 419 AYLNWIYNNWKAEL 432

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RESULT 9
US-10-199-672-330
; Sequence 330, Application US/10199672
; Publication No. US20030148442A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

```

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1  APPLICANT: Zhang, Zemin
2  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
3  TITLE OF INVENTION: ACIDS ENCODING THE SAME
4  FILE REFERENCE: P343ORICI
5  CURRENT APPLICATION NUMBER: US/10/199,672
6  CURRENT FILING DATE: 2002-07-18
7  PRIOR APPLICATION NUMBER: US/10/052,586
8  PRIOR FILING DATE: 2002-01-15
9  PRIOR APPLICATION NUMBER: 60/059263
10 PRIOR FILING DATE: 1997-09-18
11 PRIOR APPLICATION NUMBER: 60/059266
12 PRIOR FILING DATE: 1997-09-18
13 PRIOR APPLICATION NUMBER: 60/062250
14 PRIOR FILING DATE: 1997-10-17
15 PRIOR APPLICATION NUMBER: 60/063120
16 PRIOR FILING DATE: 1997-10-24
17 PRIOR APPLICATION NUMBER: 60/063121
18 PRIOR FILING DATE: 1997-10-24
19 PRIOR APPLICATION NUMBER: 60/063486
20 PRIOR FILING DATE: 1997-10-21
21 PRIOR APPLICATION NUMBER: 60/063540
22 PRIOR FILING DATE: 1997-10-28
23 PRIOR APPLICATION NUMBER: 60/063541
24 PRIOR FILING DATE: 1997-10-28
25 PRIOR APPLICATION NUMBER: 60/063544
26 PRIOR FILING DATE: 1997-10-28
27 Remaining prior application data removed - See File Wrapper or PALM.
28 NUMBER OF SEQ ID NOS: 612
29 SEQ ID NO 330
30 LENGTH: 432
31 TYPE: PRT
32 ORGANISM: Homo Sapien
33 US-10-199-672-330

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Query Match	98.1%;	Score	2297.5;	DB	12;	Length	432;
Best Local Similarity	98.8%;	Ref. No.	6.1e-222;				
Matches	429;	Conservative	0;	Mismatches	0;	Indels	5;
						Gaps	1

QY	2	DPDSQPLNSLDVPLKRP	IPMETFRKVGPIII	ALLSLASIIIVVLI	KVILDKYFL	61
DB	4	DPDSQPLNSLDVPLKRP	IPMETFRKVGPIII	ALLSLASIIIVVLI	KVILDKYFL	63
QY	62	CGQPLHFI	IPRKQLCDGELDCPL	GBDEEHCVRKSP	PEGPAVAVRLSKDRSTLQVLDSATGNW	121
DB	64	CGQPLHFI	IPRAQLCDGELDCPL	GBDEEHCVRKSP	PEGPAVAVRLSKDRSTLQVLDSATGNW	123
QY	122	FSACFDNFTEAL	EATACHROMGYSSKPT	TRAVEIGDPDQLD	VVEITENSQELMRNSSGPC	181
DB	124	FSACFDNFTEAL	EATACQMGYS----	RAVEIGDPDQLD	VVEITENSQELMRNSSGPC	178
QY	182	LSGSLVSLHCLACG	KSLSKTPRVVGGEEASVDSWP	MQVSIQYDKQHVCGSILDPHWLITA	241	
DB	179	LSGSLVSLHCLACG	KSLSKTPRVVGGEEASVDSWP	MQVSIQYDKQHVCGSILDPHWLITA	238	
QY	242	AHCFRKHTDVENW	KVRAGSDKLGSP	PPSLAVAKIIIEFN	PMYPKONDIALMKLQPLPFTS	301
DB	239	AHCFRKHTDVENW	KVRAGSDKLGSP	PPSLAVAKIIIEFN	PMYPKONDIALMKLQPLPFTS	298
QY	302	GTVRPICLPFFDEEL	TPATPLWICWG	TKTQNGKXSDILLOAS	VQVVDSTRCNADDAVQ	361
DB	299	GTVRPICLPFFDEEL	TPATPLWICWG	TKTQNGKXSDILLOAS	VQVVDSTRCNADDAVQ	358
QY	362	GEVTEKMKCAGI	PEGGVDTCCQDSG	GPLMYQSDQMHVVGIV	SWGVCGGPSPGVTYTKVS	421
DB	359	GEVTEKMKCAGI	PEGGVDTCCQDSG	GPLMYQSDQMHVVGIV	SWGVCGGPSPGVTYTKVS	418
QY	422	AYLNIWYINWKAEL	435			
DB	419	AYLNIWYINWKAEL	432			

RESULT 10
US-10-006-172A-275

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/ PRIOR FILING DATE: 1998-09-16
/ PRIOR APPLICATION NUMBER: 60/100662
/ PRIOR FILING DATE: 1998-09-16
/ PRIOR APPLICATION NUMBER: 60/100664
/ PRIOR FILING DATE: 1998-09-16
/ PRIOR APPLICATION NUMBER: 60/100693
/ PRIOR FILING DATE: 1998-09-17
/ PRIOR APPLICATION NUMBER: 60/100694
/ PRIOR FILING DATE: 1998-09-17
/ PRIOR APPLICATION NUMBER: 60/100710
/ PRIOR FILING DATE: 1998-09-17
/ PRIOR APPLICATION NUMBER: 60/100711
/ PRIOR FILING DATE: 1998-09-17
/ PRIOR APPLICATION NUMBER: 60/100848
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/ PRIOR APPLICATION NUMBER: 60/100849
/ PRIOR FILING DATE: 1998-09-18
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/ PRIOR FILING DATE: 1998-09-17
/ PRIOR APPLICATION NUMBER: 60/100930
/ PRIOR FILING DATE: 1998-09-17
/ PRIOR APPLICATION NUMBER: 60/101014
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/ PRIOR FILING DATE: 1998-09-18
/ PRIOR APPLICATION NUMBER: 60/101071
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/ PRIOR APPLICATION NUMBER: 60/101279
/ PRIOR FILING DATE: 1998-09-22
/ PRIOR APPLICATION NUMBER: 60/101471
/ PRIOR FILING DATE: 1998-09-23
/ PRIOR APPLICATION NUMBER: 60/101472
/ PRIOR FILING DATE: 1998-09-23
/ PRIOR APPLICATION NUMBER: 60/101474
/ PRIOR FILING DATE: 1998-09-23
/ PRIOR APPLICATION NUMBER: 60/101475
/ PRIOR FILING DATE: 1998-09-23
/ PRIOR APPLICATION NUMBER: 60/101476
/ PRIOR FILING DATE: 1998-09-23
/ PRIOR APPLICATION NUMBER: 60/101477
/ PRIOR FILING DATE: 1998-09-23
/ PRIOR APPLICATION NUMBER: 60/101479
/ PRIOR FILING DATE: 1998-09-23
/ PRIOR APPLICATION NUMBER: 60/101738
/ PRIOR FILING DATE: 1998-09-24
/ PRIOR APPLICATION NUMBER: 60/101741
/ PRIOR FILING DATE: 1998-09-24
/ PRIOR APPLICATION NUMBER: 60/101743
/ PRIOR FILING DATE: 1998-09-24
/ PRIOR APPLICATION NUMBER: 60/101915
/ PRIOR FILING DATE: 1998-09-24
/ PRIOR APPLICATION NUMBER: 60/101916
/ PRIOR FILING DATE: 1998-09-24
/ PRIOR APPLICATION NUMBER: 60/102207
/ PRIOR FILING DATE: 1998-09-29
/ PRIOR APPLICATION NUMBER: 60/102240
/ PRIOR FILING DATE: 1998-09-29
/ PRIOR APPLICATION NUMBER: 60/102307
/ PRIOR FILING DATE: 1998-09-29
/ PRIOR APPLICATION NUMBER: 60/102330
/ PRIOR FILING DATE: 1998-09-29
/ PRIOR APPLICATION NUMBER: 60/102331
/ PRIOR FILING DATE: 1998-09-29
/ PRIOR APPLICATION NUMBER: 60/102484
/ PRIOR FILING DATE: 1998-09-30
/ PRIOR APPLICATION NUMBER: 60/102487
/ PRIOR FILING DATE: 1998-09-30
/ PRIOR APPLICATION NUMBER: 60/102570
/ PRIOR FILING DATE: 1998-09-30
/ PRIOR APPLICATION NUMBER: 60/102571
/ PRIOR FILING DATE: 1998-09-30
/ PRIOR APPLICATION NUMBER: 60/102684
/ PRIOR FILING DATE: 1998-10-01

/ PRIOR APPLICATION NUMBER: 60/102687
/ PRIOR FILING DATE: 1998-10-01
/ PRIOR APPLICATION NUMBER: 60/102965
/ PRIOR FILING DATE: 1998-10-02
/ PRIOR APPLICATION NUMBER: 60/103258
/ PRIOR FILING DATE: 1998-10-06
/ PRIOR APPLICATION NUMBER: 60/103314
/ PRIOR FILING DATE: 1998-10-07
/ PRIOR APPLICATION NUMBER: 60/103315
/ PRIOR FILING DATE: 1998-10-07
/ PRIOR APPLICATION NUMBER: 60/103328
/ PRIOR FILING DATE: 1998-10-07
/ PRIOR APPLICATION NUMBER: 60/103395
/ PRIOR FILING DATE: 1998-10-07
/ PRIOR APPLICATION NUMBER: 60/103396
/ PRIOR FILING DATE: 1998-10-07
/ PRIOR APPLICATION NUMBER: 60/103401
/ PRIOR FILING DATE: 1998-10-07
/ PRIOR APPLICATION NUMBER: 60/103449
/ PRIOR FILING DATE: 1998-10-06
/ PRIOR APPLICATION NUMBER: 60/103633
/ PRIOR FILING DATE: 1998-10-08
/ PRIOR APPLICATION NUMBER: 60/103678
/ PRIOR FILING DATE: 1998-10-08
/ PRIOR APPLICATION NUMBER: 60/103679
/ PRIOR FILING DATE: 1998-10-08
/ PRIOR APPLICATION NUMBER: 60/103711
/ PRIOR FILING DATE: 1998-10-08
/ PRIOR APPLICATION NUMBER: 60/104257
/ PRIOR FILING DATE: 1998-10-14
/ PRIOR APPLICATION NUMBER: 60/104987
/ PRIOR FILING DATE: 1998-10-20
/ PRIOR APPLICATION NUMBER: 60/105000
/ PRIOR FILING DATE: 1998-10-20
/ PRIOR APPLICATION NUMBER: 60/105002
/ PRIOR FILING DATE: 1998-10-20
/ PRIOR APPLICATION NUMBER: 60/105104
/ PRIOR FILING DATE: 1998-10-21
/ PRIOR APPLICATION NUMBER: 60/105169
/ PRIOR FILING DATE: 1998-10-22
/ PRIOR APPLICATION NUMBER: 60/105266
/ PRIOR FILING DATE: 1998-10-22
/ PRIOR APPLICATION NUMBER: 60/105693
/ PRIOR FILING DATE: 1998-10-26
/ PRIOR APPLICATION NUMBER: 60/105694
/ PRIOR FILING DATE: 1998-10-26
/ PRIOR APPLICATION NUMBER: 60/105807
/ PRIOR FILING DATE: 1998-10-27
/ PRIOR APPLICATION NUMBER: 60/105881
/ PRIOR FILING DATE: 1998-10-27
/ PRIOR APPLICATION NUMBER: 60/105882
/ PRIOR FILING DATE: 1998-10-27
/ PRIOR APPLICATION NUMBER: 60/106023
/ PRIOR FILING DATE: 1998-10-28

Query Match 98.1%; Score 2297.5; DB 12; Length 432;
Best Local Similarity 98.8%; Pred. No. 6.1e-222;
Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 2 DPDSQPLNSLDVKPLRPRIEMETFRKVGIIIIALLSLASIIIVVLIKVILDKYFL 61
Db 4 DPDSQPLNSLDVKPLRPRIEMETFRKVGIIIIALLSLASIIIVVLIKVILDKYFL 63
QY 62 CQOPLHFIPRKOLCDGELDCPLGEDEEHCVKSFPEGPVAVRLSKDRSTLOVLDSATGNW 121
Db 64 CQOPLHFIPRKOLCDGELDCPLGEDEEHCVKSFPEGPVAVRLSKDRSTLOVLDSATGNW 123
QY 122 FSACFDNFTALAEATACRQMGYSKPTTFAVEIGDPQDLDDVVVEITENSQELMRNSSGPC 181
Db 124 FSACFDNFTALAEATACRQMGYS-----RAVEIGDPQDLDDVVVEITENSQELMRNSSGPC 178
QY 182 LSGSLVSLHCLACGKSLKTPRVVCGGEASVDSPHVNVSIOYDKQNVCGSGSLDPHWLTA 241
```


Db 179 LSGSLVSLHCLACGKSLKTRVVGGEASVDSWPQVSIQYDKQHVCGGSLDPHVLTA 238
QY 242 AHCFRKHTDVFNWKVRAGSKLGSFPPSLAVAKIIIIIFNPNPKNDIALMKLOPPLTFS 301
Db 239 AHCFRKHTDVFNWKVRAGSKLGSFPPSLAVAKIIIIIFNPNPKNDIALMKLOPPLTFS 298
QY 302 GTVRPICLPFFDEELTPATPLWIIIGWFTKONGGKMSDILLQASVQVIDSTRCNADDAAYQ 361
Db 299 GTVRPICLPFFDEELTPATPLWIIIGWFTKONGGKMSDILLQASVQVIDSTRCNADDAAYQ 358
QY 362 GEVTEKMCAGIPGEGVDTCCGDSGGLMYQSDQHVHVGIVSWGCGGPGSTPGVYTKVS 421
Db 359 GEVTEKMCAGIPGEGVDTCCGDSGGLMYQSDQHVHVGIVSWGCGGPGSTPGVYTKVS 418
QY 422 AYLNNWYNNVWKAEL 435
Db 419 AYLNNWYNNVWKAEL 432

RESULT 11
US-10-187-749-330
; Sequence 330, Application US/10187749
; Publication No. US20030153036A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/187,749
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 330
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-187-749-330

Query Match 98.1%; Score 2297.5; DB 12; Length 432;
Best Local Similarity 98.8%; Pred. No. 6.1e-222;
Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
QY 2 DPDSQPLNSLDVKEPKRIPMETFRKVGIPIIIALLSLASHIIIVVILKILDKYVFL 61

Db 4 DPDSQPLNSLDVKEPKRIPMETFRKVGIPIIIALLSLASHIIIVVILKILDKYVFL 63
QY 62 CGOPLHPIPRKQICDGLDCPLGEDEHCVKSPPEGPAVAVRLSKDRSTLQVLDSATGNW 121
Db 64 CGOPLHPIPRKQICDGLDCPLGEDEHCVKSPPEGPAVAVRLSKDRSTLQVLDSATGNW 123
QY 122 FSACFDNFTALAEACROMGYSSKPTFRAVEIGDPDQDLVDVEITENSQELRMENSSGPC 181
Db 124 FSACFDNFTALAEACROMGYSSKPTFRAVEIGDPDQDLVDVEITENSQELRMENSSGPC 178
QY 182 LSGSLVSLHCLACGKSLKTRVVGGEASVDSWPQVSIQYDKQHVCGGSLDPHVLTA 241
Db 179 LSGSLVSLHCLACGKSLKTRVVGGEASVDSWPQVSIQYDKQHVCGGSLDPHVLTA 238
QY 242 AHCFRKHTDVFNWKVRAGSKLGSFPPSLAVAKIIIIIFNPNPKNDIALMKLOPPLTFS 301
Db 239 AHCFRKHTDVFNWKVRAGSKLGSFPPSLAVAKIIIIIFNPNPKNDIALMKLOPPLTFS 298
QY 302 GTVRPICLPFFDEELTPATPLWIIIGWFTKONGGKMSDILLQASVQVIDSTRCNADDAAYQ 361
Db 299 GTVRPICLPFFDEELTPATPLWIIIGWFTKONGGKMSDILLQASVQVIDSTRCNADDAAYQ 358
QY 362 GEVTEKMCAGIPGEGVDTCCGDSGGLMYQSDQHVHVGIVSWGCGGPGSTPGVYTKVS 421
Db 359 GEVTEKMCAGIPGEGVDTCCGDSGGLMYQSDQHVHVGIVSWGCGGPGSTPGVYTKVS 418
QY 422 AYLNNWYNNVWKAEL 435
Db 419 AYLNNWYNNVWKAEL 432

RESULT 12
US-10-194-457-330
; Sequence 330, Application US/10194457
; Publication No. US20030153037A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C296
; CURRENT APPLICATION NUMBER: US/10/194,457
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 330

; LENGTH: 432

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-194-457-330

Query Match 98.1%; Score 2297.5; DB 12; Length 432;
Best Local Similarity 98.8%; Pred. No. 6.1e-222;
Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
QY 2 DPDSQPLNSLDVPLKRPIMPETFRKVGIPPIIALLSLASIIIVVLIKVLIDKYFL 61
Db 4 DPDSQPLNSLDVPLKRPIMPETFRKVGIPPIIALLSLASIIIVVLIKVLIDKYFL 63
QY 62 CGOPLHFTPRKQCDGELDCPLGEDEEHCVKSPFPGPAVAVRLSKDRSTLQVLD SATGNW 121
Db 64 CGOPLHFTPRKQCDGELDCPLGEDEEHCVKSPFPGPAVAVRLSKDRSTLQVLD SATGNW 123
QY 122 FSACFDNFTALAEATACRMGYSSKPTFRAVEIGDPDQDLDVVEITENSQELMRNSSGPC 181
Db 124 FSACFDNFTALAEATACRMGYSSKPTFRAVEIGDPDQDLDVVEITENSQELMRNSSGPC 178
QY 182 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSLDHPHWLTA 241
Db 179 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSLDHPHWLTA 238
QY 242 AHCFRKHTDVENWVKRAGSDKLGSPSLAVAKIIIEENPMYPKNDIALMKLOPELTF 301
Db 239 AHCFRKHTDVENWVKRAGSDKLGSPSLAVAKIIIEENPMYPKNDIALMKLOPELTF 298
QY 302 GTVRPICLPFFDEELTPATPLIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAAYQ 361
Db 299 GTVRPICLPFFDEELTPATPLIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAAYQ 358
QY 362 GEVTERKMCAGIPGEGVDTCQDSGGPLMYQSDQHVHVGIVSWGCGGPGSTPGVYTKVS 421
Db 359 GEVTERKMCAGIPGEGVDTCQDSGGPLMYQSDQHVHVGIVSWGCGGPGSTPGVYTKVS 418
QY 422 AYLNWIYVWKAEL 435
Db 419 AYLNWIYVWKAEL 432

RESULT 13

US-10-184-642-330

; Sequence 330, Application US/10184642

; Publication No. US20030157835A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C194

; CURRENT APPLICATION NUMBER: US/10/184,642

; CURRENT FILING DATE: 2002-06-27

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 330

; LENGTH: 432

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-184-642-330

Query Match 98.1%; Score 2297.5; DB 12; Length 432;

Best Local Similarity 98.8%; Pred. No. 6.1e-222;

Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 2 DPDSQPLNSLDVPLKRPIMPETFRKVGIPPIIALLSLASIIIVVLIKVLIDKYFL 61
Db 4 DPDSQPLNSLDVPLKRPIMPETFRKVGIPPIIALLSLASIIIVVLIKVLIDKYFL 63
QY 62 CGOPLHFTPRKQCDGELDCPLGEDEEHCVKSPFPGPAVAVRLSKDRSTLQVLD SATGNW 121
Db 64 CGOPLHFTPRKQCDGELDCPLGEDEEHCVKSPFPGPAVAVRLSKDRSTLQVLD SATGNW 123
QY 122 FSACFDNFTALAEATACRMGYSSKPTFRAVEIGDPDQDLDVVEITENSQELMRNSSGPC 181
Db 124 FSACFDNFTALAEATACRMGYSSKPTFRAVEIGDPDQDLDVVEITENSQELMRNSSGPC 178
QY 182 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSLDHPHWLTA 241
Db 179 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSLDHPHWLTA 238
QY 242 AHCFRKHTDVENWVKRAGSDKLGSPSLAVAKIIIEENPMYPKNDIALMKLOPELTF 301
Db 239 AHCFRKHTDVENWVKRAGSDKLGSPSLAVAKIIIEENPMYPKNDIALMKLOPELTF 298
QY 302 GTVRPICLPFFDEELTPATPLIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAAYQ 361
Db 299 GTVRPICLPFFDEELTPATPLIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAAYQ 358
QY 362 GEVTERKMCAGIPGEGVDTCQDSGGPLMYQSDQHVHVGIVSWGCGGPGSTPGVYTKVS 421
Db 359 GEVTERKMCAGIPGEGVDTCQDSGGPLMYQSDQHVHVGIVSWGCGGPGSTPGVYTKVS 418
QY 422 AYLNWIYVWKAEL 435
Db 419 AYLNWIYVWKAEL 432

RESULT 14

US-10-196-747-330

; Sequence 330, Application US/10196747

; Publication No. US20030162250A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C346

; CURRENT APPLICATION NUMBER: US/10/196,747

; CURRENT FILING DATE: 2002-07-15

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 330

; LENGTH: 432

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-196-747-330

Query Match 98.1%; Score 2297.5; DB 12; Length 432;

Best Local Similarity 98.8%; Pred. No. 6.1e-222;

Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 2 DPDSQPLNSLDVPLKRPIMPETFRKVGIPPIIALLSLASIIIVVLIKVLIDKYFL 61

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Db 4 DPDSQPLNSLDVVKLRKPRIPMETFRKVGPIIIALLSLASIIIVVVLKIVLDKYYFL 63
Qy 62 CGQPLHFIIPRKQLCDGELDCPLGDEEHCVKSFPEGPAVAVRLSKDRSTLQVLD SATGNW 121
Db 64 CGQPLHFIIPRKQLCDGELDCPLGDEEHCVKSFPEGPAVAVRLSKDRSTLQVLD SATGNW 123
Qy 122 FSACFDNFTALAEATACROMGYSKPTFRAVEIGDPQDLVDVEITENSQELMRNSSGPC 181
Db 124 FSACFDNFTALAEATACROMGYS-----RAVEIGDPQDLVDVEITENSQELMRNSSGPC 178
Qy 182 LSGSLVSLHCLACGSKLTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSILDPHWLTA 241
Db 179 LSGSLVSLHCLACGSKLTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSILDPHWLTA 238
Qy 242 AHCFRKHDTVNNKVRAGSKLGFPPSLAVAKIIIEFNPMYPKNDIALMKLOPPLTFS 301
Db 239 AHCFRKHDTVNNKVRAGSKLGFPPSLAVAKIIIEFNPMYPKNDIALMKLOPPLTFS 298
Qy 302 GTVRPICLPFPDEELTPATPLWIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAAYQ 361
Db 299 GTVRPICLPFPDEELTPATPLWIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAAYQ 358
Qy 362 GEVTEKMKCAGIPGEGVDTCQDGGGGLMYQSDQWHVVGIVSWGVCGGPSTPGVYTKVS 421
Db 359 GEVTEKMKCAGIPGEGVDTCQDGGGGLMYQSDQWHVVGIVSWGVCGGPSTPGVYTKVS 418
Qy 422 AYLNIWYNNWKAEL 435
Db 419 AYLNIWYNNWKAEL 432

RESULT 15
US-10-015-392A-275
; Sequence 275. Application US/10015392A
; Publication No. US20030166901A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC58
; CURRENT APPLICATION NUMBER: US/10/015,392A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
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; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 275
; LENGTH: 432
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; ORGANISM: Homo sapiens
; TYPE: PRT
US-10-015-392A-275
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Query Match 98.1%; Score 2297.5; DB 12; Length 432;
Best Local Similarity 98.8%; Pred. No. 6.1e-222;
Matches 429; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
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```
Qy 2 DPDSQPLNSLDVVKLRKPRIPMETFRKVGPIIIALLSLASIIIVVVLKIVLDKYYFL 61
Db 4 DPDSQPLNSLDVVKLRKPRIPMETFRKVGPIIIALLSLASIIIVVVLKIVLDKYYFL 63
Qy 62 CGQPLHFIIPRKQLCDGELDCPLGDEEHCVKSFPEGPAVAVRLSKDRSTLQVLD SATGNW 121
Db 64 CGQPLHFIIPRKQLCDGELDCPLGDEEHCVKSFPEGPAVAVRLSKDRSTLQVLD SATGNW 123
Qy 122 FSACFDNFTALAEATACROMGYSKPTFRAVEIGDPQDLVDVEITENSQELMRNSSGPC 181
Db 124 FSACFDNFTALAEATACROMGYS-----RAVEIGDPQDLVDVEITENSQELMRNSSGPC 178
Qy 182 LSGSLVSLHCLACGSKLTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSILDPHWLTA 241
Db 179 LSGSLVSLHCLACGSKLTPRVVGGEEASVDSWPQVSIQYDKQHVCGGSILDPHWLTA 238
Qy 242 AHCFRKHDTVNNKVRAGSKLGFPPSLAVAKIIIEFNPMYPKNDIALMKLOPPLTFS 301
Db 239 AHCFRKHDTVNNKVRAGSKLGFPPSLAVAKIIIEFNPMYPKNDIALMKLOPPLTFS 298
Qy 302 GTVRPICLPFPDEELTPATPLWIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAAYQ 361
Db 299 GTVRPICLPFPDEELTPATPLWIIGWFTKQNGKMSDILLQASVQVIDSTRCNADDAAYQ 358
Qy 362 GEVTEKMKCAGIPGEGVDTCQDGGGGLMYQSDQWHVVGIVSWGVCGGPSTPGVYTKVS 421
Db 359 GEVTEKMKCAGIPGEGVDTCQDGGGGLMYQSDQWHVVGIVSWGVCGGPSTPGVYTKVS 418
Qy 422 AYLNIWYNNWKAEL 435
Db 419 AYLNIWYNNWKAEL 432
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Search completed: December 2, 2003, 02:51:18
Job time : 325.904 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2003, 00:14:04 ; Search time 31.7125 Seconds
(without alignments)
580.377 Million cell updates/sec

Title: US-09-607-745-2

Perfect score: 2342

Sequence: 1 MDPDSQPLNSLDVKPLRKP.....VYTKVSAYLNWYNNVKAEL 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCRTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2338	99.8	435	3	US-09-008-271A-6
2	2196	93.8	423	4	US-09-656-002-2
3	676.5	28.9	492	3	US-09-342-749-2
4	676.5	28.9	492	4	US-09-691-840-2
5	655.5	28.0	454	3	US-09-518-046-2
6	588.5	25.1	417	4	US-09-820-002-4
7	584	24.9	455	3	US-09-261-416-2
8	580	24.8	376	4	US-09-820-002-2
9	574	24.5	416	2	US-09-000-846-2
10	571	24.4	798	5	US-08-200-900A-2
11	571	24.4	798	5	PCT-US94-00616-2
12	568	24.3	418	1	US-08-508-448C-25
13	568	24.3	418	4	US-09-370-838-82
14	568	24.3	418	4	US-09-370-838-83
15	566	24.2	418	4	US-09-370-838-82
16	558.5	23.8	283	3	US-08-807-151-1
17	558.5	23.8	283	4	US-09-478-957-1
18	531.5	22.7	232	1	US-08-508-448C-19
19	512.5	21.9	256	2	US-09-027-337-3
20	512.5	21.9	256	4	US-09-644-600-3
21	511	21.8	638	2	US-08-681-151-3
22	507.5	21.7	255	3	US-08-944-483-67
23	503.5	21.5	285	4	US-09-023-942A-26
24	486	20.8	248	3	US-08-944-483-63
25	483	20.6	314	4	US-09-023-942A-6
26	482.5	20.6	284	4	US-09-387-375-7
27	478	20.4	314	3	US-09-008-271A-3

28	477	20.4	312	4	US-09-023-942A-4	Sequence 4, Appli
29	475	20.3	407	4	US-09-734-675-4	Sequence 4, Appli
30	472.5	20.2	317	4	US-09-386-829-7	Sequence 7, Appli
31	470	20.1	902	4	US-09-644-600-10	Sequence 10, Appli
32	467.5	20.0	290	4	US-09-386-653A-7	Sequence 7, Appli
33	466.5	19.9	405	4	US-09-734-675-2	Sequence 2, Appli
34	465.5	19.9	250	3	US-08-944-483-68	Sequence 68, Appli
35	463	19.8	855	2	US-09-027-337-2	Sequence 2, Appli
36	463	19.8	855	4	US-09-644-600-2	Sequence 2, Appli
37	458.5	19.6	316	4	US-09-387-375-9	Sequence 9, Appli
38	458.5	19.6	790	4	US-08-991-761A-13	Sequence 13, Appli
39	455.5	19.4	812	1	US-08-248-629A-1	Sequence 1, Appli
40	455.5	19.4	812	1	US-08-451-932-1	Sequence 1, Appli
41	455.5	19.4	812	1	US-08-452-260-1	Sequence 1, Appli
42	455.5	19.4	812	1	US-08-326-785-1	Sequence 1, Appli
43	455.5	19.4	812	2	US-08-612-788-1	Sequence 1, Appli
44	455.5	19.4	812	2	US-08-605-598B-1	Sequence 1, Appli
45	455.5	19.4	812	2	US-08-429-743-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-008-271A-6
; Sequence 6, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNOT13
; CLONE: 1337018
; SEQUENCE DESCRIPTION: SEQ ID NO: 6 :
US-09-008-271A-6

Query Match 99.8%; Score 2338; DB 3; Length 435;
Best Local Similarity 99.8%; Pred. No. 6.2e-231;
Matches 434; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPSDQPLNSLDVFKLPRIPMETFRKVGPIIIIALSLASIIIVVLKVIDKYIF 60
DB 1 MDPSDQPLNSLDVFKLPRIPMETFRKVGPIIIIALSLASIIIVVLKVIDKYIF 60

QY 61 LCGQPLHFTPRKOLCGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLD SATCN 120
DB 61 LCGQPLHFTPRKOLCGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLD SATCN 120

QY 121 WFSACPDNTEALAEACRQMGYSKPTTFRIVEIGPDQDLVDVVEITENSQELMRNNSGP 180
DB 121 WFSACPDNTEALAEACRQMGYSKPTTFRIVEIGPDQDLVDVVEITENSQELMRNNSGP 180

QY 181 CLSGSLVSLHCLACGSLKTPRVVVGEEASVDSWPMQVSIQYDKQHVCGSILDPHWLT 240
DB 181 CLSGSLVSLHCLACGSLKTPRVVVGEEASVDSWPMQVSIQYDKQHVCGSILDPHWLT 240

QY 241 AAHCFRKHDTDFVFNKVRAGSKLSPSLAVAKIIIEFNPMYPKNDIALMKLOPPLTF 300
DB 241 AAHCFRKHDTDFVFNKVRAGSKLSPSLAVAKIIIEFNPMYPKNDIALMKLOPPLTF 300

QY 301 SGTVRPCLPFDEELTPATPLWIIWGFTKQNGKMSDILLQASVQVIDSTRCNADDA 360
DB 301 SGTVRPCLPFDEELTPATPLWIIWGFTKQNGKMSDILLQASVQVIDSTRCNADDA 360

QY 361 QBEVTEKMKCAGIPGEGVDTCCGSDGGLMYQSDQHVVGIVSWGCGGSPTPGYVTKV 420
DB 361 QBEVTEKMKCAGIPGEGVDTCCGSDGGLMYQSDQHVVGIVSWGCGGSPTPGYVTKV 420

QY 421 SAYLNNIYNVWKAE 435
DB 421 SAYLNNIYNVWKAE 435

RESULT 2
US-09-656-002-2
; Sequence 2, Application US/09656002
; Patent No. 6455668
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
; FILE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; CURRENT APPLICATION NUMBER: US/09/656,002
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/525,993
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 09/493,444
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US 00/07044
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-656-002-2

Query Match 93.8%; Score 2196; DB 4; Length 423;
Best Local Similarity 97.1%; Pred. No. 2.1e-216;
Matches 408; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 16 PLRKPRIPIETFRKVGIPPIIIALLSLASIIIVVLKVIDKYIFLCGQPLHPIFRKQIC 75
DB 4 PCANPVSPPWRSSVGIPIIIALLSLASIIIVVLKVIDKYIFLCGQPLHPIFRKQIC 63

QY 76 DGEELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLD SATGNFWSACPDNFTALAE 135
DB 64 DGEELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLD SATGNFWSACPDNFTALAE 123

QY 136 TACRQMGYSKPTTFRIVEIGPDQDLVDVVEITENSQELMRNNSGCLSGSLVSLHCLAG 195
DB 124 TACRQMGYSKPTTFRIVEIGPDQDLVDVVEITENSQELMRNNSGCLSGSLVSLHCLAG 183

QY 196 KSLKTPRVVVGEEASVDSWPMQVSIQYDKQHVCGSILDPHWLTAAHCFRKHDTDFVFNK 255
DB 184 KSLKTPRVVVGEEASVDSWPMQVSIQYDKQHVCGSILDPHWLTAAHCFRKHDTDFVFNK 243

QY 256 VRAGSKLSPSLAVAKIIIEFNPMYPKNDIALMKLOPPLTFSGTVRPICLPFDEE 315
DB 244 VRAGSKLSPSLAVAKIIIEFNPMYPKNDIALMKLOPPLTFSGTVRPICLPFDEE 303

QY 316 LTPATPLWIIWGFTKQNGKMSDILLQASVQVIDSTECNADDAQOGEVTEKMKCAGIPE 375
DB 304 LTPATPLWIIWGFTKQNGKMSDILLQASVQVIDSTECNADDAQOGEVTEKMKCAGIPE 363

QY 376 GGVDTCCGSDGGLMYQSDQHVVGIVSWGCGGSPTPGYVTKVSAYLNNIYNVWKAE 435
DB 364 GGVDTCCGSDGGLMYQSDQHVVGIVSWGCGGSPTPGYVTKVSAYLNNIYNVWKAE 423

RESULT 3
US-09-342-749-2
; Sequence 2, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMRSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/342,749
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 60/091,044
; EARLIER FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-342-749-2

Query Match 28.9%; Score 676.5; DB 3; Length 492;
Best Local Similarity 39.1%; Pred. No. 1.2e-60;
Matches 150; Conservative 57; Mismatches 128; Indels 49; Gaps 13;

QY 75 CDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLD SATGNFWSACPDNFTALAE 134
DB 133 CDGSHCHGEGDENRCVRLY--GP-----NFILQVSSQKSWHPVCOODWNNYNG 181

QY 135 ETACRQMGYSKPTTFRIVEIGPDQDLVDVVEITENSQELMRNNSG-----PCL 182
DB 182 RAACHDMGY--KNPFYSSQ-----GIVDDSGSTSFMKLNTSAGNVIIYKLYHSDACS 232

QY 183 SGSLVSLHCLACGSL-----KTPRVVVGEEASVDSWPMQVSIQYDKQHVCGSILDPHWLT 239
DB 233 SKAVVSLRCIACGVNLNRSRQSRIVGGESALPGAMPQVSLHVQNVHVHVCSSIIITPEWIV 292

QY 240 TAAHCFRKH--TDVFNKVRAGSKLSP-----PSLAVAKIIIEFNPMY---PKNDIAL 291
DB 293 TAAHCFRKH--TDVFNKVRAGSKLSP-----PSLAVAKIIIEFNPMY---PKNDIAL 291

QY 292 MKLOPPLTFSGTVRPICLPFDEELTPATPLWIIWGFTKQNGKMSDILLQASVQVIDS 351
DB 349 MKLOPPLTFSGTVRPICLPFDEELTPATPLWIIWGFTKQNGKMSDILLQASVQVIDS 351

QY 352 TRCNADDAQOGEVTEKMKCAGIPGEGVDTCCGSDGGLMYQSDQ--WHVVGIVSWGCGG 410

Db 408 QRCNSRYVDNLITPAMICAGFLQGNVDSQDGGPLVTSKNNIWLIGDTSWGSCAK 467
QY 411 PSTPGVYTKVSAYLNWYINWKAEL 434
Db 468 AYRPGVYGNWVFTDWIYRQVRAD 491

RESULT 4

US-09-691-840-2
; Sequence 2, Application US/09691840
; Patent No. 6444419
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-P.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMRSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/691,840
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US/09/342,749
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/091,044
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-691-840-2

Query Match 28.9%; Score 676.5; DB 4; Length 492;
Best Local Similarity 39.1%; Pred. No. 1.2e-60;
Matches 150; Conservative 57; Mismatches 128; Indels 49; Gaps 13;
QY 75 CDGELDCPLGDEBEHCVKSPPEGPAVAVRLSKDRSTLQVLDSATGNWFSACDFNFTTEALA 134
Db 133 CDGVSHCPGDEENRCVRLY--GP-----NFILOVYSSQEKSHWPCQDDWNNYNG 181
QY 135 ETACROMGYSKPTTFAVEIGPDQDLVDVEITENSQELRMENSSG-----PCL 182
Db 182 RAACRDMGY--KNNFYSSQ-----GIVDSSGTSFPMKNTSAGNVDIYKLYVHSDACS 232
QY 183 SGLSVSLHCLACGKSL---KTPRVVGGEASVDSWPQVSIQYDKQHVCGGSLDPHWL 239
Db 233 SKAVSLURCLACGVNLNSRQSRIVGGSALPGAWPQVSLHVQNVHVCVCGGSIITPEWIV 292
QY 240 TAAHCFRKH--TDVFNWVKRAGSKLSF---PSLAVAKIIIEFNPY---PKNDIAL 291
Db 293 TAAHCFVEKPLNPNWHTAFAGILR-QSFMFYGAGYQVEKVI---SHENYDKTKNDIAL 348
QY 292 MKLQPLTFSGTVRPICLPFDFDELTATPLWIIIGWFTKONGKMSDILLQASVQVIDS 351
Db 349 MKLQKELTFNDLVKVPCLPFGMMQLPEQLCWISGWGATEBK-GKTSEVLNAAKVLIIET 407
QY 352 TRCNADDAVQGEVTEKMCACAGIPEGVDTCQDGGGGLMYQSDQ--WHVVGIVSWGYCGCG 410
Db 408 QRCNSRYVDNLITPAMICAGFLQGNVDSQDGGGGLVTSKNNIWLIGDTSWGSCAK 467

QY 411 PSTPGVYTKVSAYLNWYINWKAEL 434
Db 468 AYRPGVYGNWVFTDWIYRQVRAD 491

RESULT 5

US-09-518-046-2
; Sequence 2, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.

; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 2
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: complete amino acid sequence of TADG-12
; OTHER INFORMATION: protein
US-09-518-046-2

Query Match 28.0%; Score 655.5; DB 3; Length 454;
Best Local Similarity 35.7%; Pred. No. 1.5e-58;
Matches 158; Conservative 73; Mismatches 149; Indels 63; Gaps 18;
QY 22 IPMETPRKVGIFIIIIALLSLASIIIVVLIKVLID---KY-----YFLCGOPLHFIPIKQL 74
Db 44 LPFEVFSQSSSLGIITL-----ILALAIGLIHFDGSGKYRCSSPKC---IELITR--- 92
QY 75 CDGELDCPLGDEBEHCVKSPPEGPAVAVRLSKDRSTLQVLDSATGNWFSACDFNFTTEALA 134
Db 93 CDGVSDCKGDEYRC-----VRVGGONAVLQVFTAA--SWKTMCSDDWKGHYA 139
QY 135 ETACROMGYSS-----KPTTFAVEIGPDQDLVDVEITENSQELRMENSSGPPCL 182
Db 140 NVACAQLGFPYSVSSDNLVSSLEGQFREFFVSIDHLLPDDKVTALHSHVYVREG---CA 196
QY 183 SGLSVSLHCLACG--KSLKTPRVVGGEASVDSWPQVSIQYDKQHVCGGSLDPHWLTA 241
Db 197 SGHVVTLOCTACGHRGYSRIVGGNMSLLSQWPQASLQFGYHLGCGSVITPLMIITA 256
QY 242 AHCFRKHITDVF---NWKVRAGSKL--GSFPSLAVAKIIIEFNPY--PK--DNDIALMK 293
Db 257 AHCV---YDYLPKSWTIQVGLVSLDNPAPSHLVEKIV---YHSYKPKRLGNDIALMK 310
QY 294 LOFFPLTFSGTVRPICLPFDFDELTATPLWIIIGWFTKONGKMSDILLQASVQVIDSTR 353
Db 311 LAGPLTFNEMIQVCLPNSSENFPPDGKVCWTSGWAT--EDGDASPVLNHAAVPLISNKI 369
QY 354 CNADDAVQGEVTEKMCACAGIPEGVDTCQDGGGGLMYQSDQ--WHVVGIVSWGYCGGGS 412
Db 370 CNHRDVGIGIISPSMLCAGYLTGGVDSQDGGGGLVQCOERRLWKLIVGATSFYGICAEVN 429
QY 413 TPGVYTKVSAYLNWYINWKAEL 435
Db 430 KPGVYTRVTSFLDWIHEQMERDL 452

RESULT 6

US-09-820-002-4
; Sequence 4, Application US/09820002
; Patent No. 6482630
; GENERAL INFORMATION:
; APPLICANT: Gan, Weinui
; APPLICANT: Ye, Jane
; APPLICANT: DiFrancesco, Valentina
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001194
; CURRENT APPLICATION NUMBER: US/09/820,002
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 417

Db 177 FAGAVASPHGLQLGVAVVYHGGYLPFRDPNSSENSNDIALVHLSPLTEYIQPVC 236
QY 309 LPFDEBELPATPLWIGFTYKONGKMSDILLQASVQVIDTRCNADDAIYQCEVTEKM 368
Db 237 LPAAGQALVDGKICTVTWGNT-QYTGQAGVLQEARVPIISNDVNCNADFYGNQIKPKM 295
QY 369 MCAGIPBGGVDTCQDGGGGLMYQ-----SDQHWVGVIVSGVGGGPGSPFPYVYTKVSAY 423
Db 296 FCAGYEGGIDAQDGGGGFVCEDSISRTPRWELCGIVSGWGTGCALAQKPGYVYTKVSDF 355
QY 424 LNWYVNWK 432
Db 356 REWIFQAIK 364

RESULT 9

US-09-000-846-2
; Sequence 2, Application US/09000846
; Patent No. 5981830
; GENERAL INFORMATION:
; APPLICANT: WU, QINGYU
; APPLICANT: SADLER, JASPER
; TITLE OF INVENTION: KNOCKOUT MICE AND THEIR PROGENY WITH
; TITLE OF INVENTION: DISRUPTED SERINE PROTEASE GENES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/000,846
; FILING DATE: 30-DEC-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/866,058
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: LEBOVITZ, RICHARD M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: BERLX 65P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-000-846-2
Query Match 24.5%; Score 574; DB 2; Length 416;
Best Local Similarity 30.8%; Pred. No. 3e-50;
Matches 135; Conservative 62; Mismatches 151; Indels 90; Gaps 10;
QY 30 VGPIIALLSLAGIIIVVLKIVLKYFLCQPLHFTPRKQLCDGELDCPLGEDEEH 89
Db 22 VGTLLFTLGIGAASWAIIVTILLQ-----SDQE- 48
QY 90 CVKSFEPGPAVAVRLSKDRSTLQVLDGATGNWFSACFDNFTALAEATACROMGY----- 143
Db 49 -----PLYQVQLSPGDSLAIVDFDKTEGWRLLCSSRSNARVAGLGCBEWGFRLAH 100
QY 144 -----SSKPTFRAVEIG-----PDQDLDDVVEITENSQELMRNSSGGCLSGSLVSL 189

Db 101 SELDVRTAGANGTSFGFCVDEGGLRLAQRLLDVIVSVD-----CPRGRFLTA 147
QY 190 HCLACG-KSLKTPRVVGGEEASVDSWFPWQVSTQYDKQHVCGSILDPHWVLTAAHCFRKH 248
Db 148 TCQDCGRRLFLPDRIVGGQDSSLGRWPMQVSLRYDGTHLGSGSLSGDWLVTAAHCFPER 207
QY 249 TDVEN-WKVRAGSDKLGSPSLAVAKIIIEFNPMYP-----KDNIDIALMKLOPPLT 299
Db 208 NRVLSRWRFVFAAVARTSFAVQLGVQAVIYHGGYLPFRDPTIDENSNDIALVHLSLSP 267
QY 300 FSGTVRPICLPFPDEBELPATPLWIGFTYKONGKMSDILLQASVQVIDTRCNADDA 359
Db 268 LTEYIQEVLCPAAGQALVDGKICTVTWGNT-QYTGQAGVLQEARVPIISNEVCNPDF 326
QY 360 YQCEVTEKMKCAGIPBGGVDTCQDGGGGLMYQ-----SDQHWVGVIVSGVGGGPGSP 414
Db 327 YGNQIKPRMFCAGYEGGIDAQDGGGGFVCEDSISGTSRWRLCGIVSGWGTGCALARKP 386
QY 415 GVYTKVSAYLNIYVNWK 432
Db 387 GVYTKVDFREWIFQAIK 404

RESULT 10

US-08-200-900A-2
; Sequence 2, Application US/08200900A
; Patent No. 5665566
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. - Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,900A
; FILING DATE: 23-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinert, Maureen C.
; REGISTRATION NUMBER: 31,544
; REFERENCE/DOCKET NUMBER: GI 5201-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170 X8574
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 798 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-200-900A-2

Query Match 24.4%; Score 571; DB 1; Length 798;
Best Local Similarity 35.0%; Pred. No. 1.6e-49;
Matches 133; Conservative 67; Mismatches 138; Indels 42; Gaps 15;
QY 69 IPRKQLDCDELCPLGDEDEHCVKSPPEGPAVAVRLSKDRSTLQVLDGATGNWFSACFDN 128
Db 435 IPIVNLCDGPPHCKDGSDEAHCVRLF-NGTDSGLVQFR--IQSI-----HWVACEN 485
QY 129 FTEALAEATACROMGY-----SSKPTFRAVEIGPQDLDVVE-----ITENSQELMRNSSGP 180

Db 486 WTTQISDDVCCQLLGLTGNSSVPT- STGGGYPVNLNTAPNGSLILTPSQ----- 535
Qy 181 CLSGSLVSLHC--LACGKSLKT-----PRVVGEEASVDSWPQVSIQYDKQHVCGSILD 234
Db 536 CLEDSLILLCQNYKSCGKKLVTEQVSPKIVGSDSGREGAPWVVALYFDQDQVCGASLVS 595
Qy 235 PHWLTAAHC-FRKHTDVFNKVRAGSKLGSF--PSLAVAKIIIEFNPMY---PKND 288
Db 596 RDWLVSAAHCYVGRNMEPSKWKAVLGLHMASNLTSFQIETRLIDQIVINPHYNKRRKND 655
Qy 289 IALMKLQFLPFTSGVTRPCLPFPDEELTPATFLWIGWFTKQNGKMSDILLOASVQV 348
Db 656 IAMHELEKVNVDYIQICLPEENQVFPFGKICSIAGNGLIYO-GSTADVLEQADVPL 714
Qy 349 IDSTRCNADDAQGEVTEKMKCAGIPGEGVDTCQDGGGPLYQ-SDQWHVVGIVSWG 407
Db 715 LSNEKCO-QOMPEYNITENMVCAGYAGVDSQDGGPLMCQENNRWLLAGVTSFGYQ 773
Qy 408 CGGPSTGVTYKVSAYLNI 427
Db 774 CALPNRPGVYARVPRFTWI 793

RESULT 11

PCT-US94-00616-2
; Sequence 2, Application PC/TUS9400616
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
; NUMBER OF SEQUENCES: 33
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00616
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 798 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-00616-2

Query Match 24.4%; Score 571; DB 5; Length 798;
Best Local Similarity 35.0%; Pred. No. 1.6e-49;
Matches 133; Conservative 67; Mismatches 138; Indels 42; Gaps 15;

Qy 69 IPRKOLCDGELPCPLGEDEEHCVKSPFEGFAVAVRLSKDRSTLQVLDGATGNWFSACFDN 128
Db 435 IFLVNLCDGFPCHKDGSDEAHCVRLF-NGTDDSGLVQPR--IQSI-----WHVACAEN 485
Qy 129 FTEALAEATACROMGY-----SSKPTTRAVEIGDPQDLVVE-----ITENSQELMRNMSGP 180
Db 486 WTTQISDDVCCQLLGLTGNSSVPT- STGGGYPVNLNTAPNGSLILTPSQ----- 535
Qy 181 CLSGSLVSLHC--LACGKSLKT-----PRVVGEEASVDSWPQVSIQYDKQHVCGSILD 234
Db 536 CLEDSLILLCQNYKSCGKKLVTEQVSPKIVGSDSGREGAPWVVALYFDQDQVCGASLVS 595
Qy 235 PHWLTAAHC-FRKHTDVFNKVRAGSKLGSF--PSLAVAKIIIEFNPMY---PKND 288
Db 596 RDWLVSAAHCYVGRNMEPSKWKAVLGLHMASNLTSFQIETRLIDQIVINPHYNKRRKND 655
Qy 289 IALMKLQFLPFTSGVTRPCLPFPDEELTPATFLWIGWFTKQNGKMSDILLOASVQV 348
Db 656 IAMHELEKVNVDYIQICLPEENQVFPFGKICSIAGNGLIYO-GSTADVLEQADVPL 714
Qy 349 IDSTRCNADDAQGEVTEKMKCAGIPGEGVDTCQDGGGPLYQ-SDQWHVVGIVSWG 407

Db 715 LSNEKCO-QOMPEYNITENMVCAGYAGVDSQDGGPLMCQENNRWLLAGVTSFGYQ 773
Qy 408 CGGPSTGVTYKVSAYLNI 427
Db 774 CALPNRPGVYARVPRFTWI 793

RESULT 12

US-08-508-448C-25
; Sequence 25, Application US/08508448C
; Patent No. 5804410
; GENERAL INFORMATION:
; APPLICANT: Kazuyoshi YAMAKA et al.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING
; TITLE OF INVENTION: TRYPSIN-LIKE ENZYME AND PROCESS FOR PRODUCING THE ENZYME
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,448C
; FILING DATE: July 28, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 418 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-508-448C-25

Query Match 24.3%; Score 568; DB 1; Length 418;
Best Local Similarity 32.4%; Pred. No. 1.2e-49;
Matches 138; Conservative 79; Mismatches 149; Indels 60; Gaps 14;

Qy 33 PIITALLSLASIIIVVLIKVLKDYFLCQQLHFTPRK--QLCDGLDCLP----- 83
Db 16 PYVVCVIVAGVWLLAVTIALLV---YFLAPDQKSYFVRSGFQLLNVEYNSQLNSPATQE 72
Qy 84 -----GEDEEHCVKSPFEG-----PAVAVRLSKD-----RSTLQVLDGATGNWFSACFD 127
Db 73 YRTLSGRIEISLITTKFESNLNRNQFIRAHVAKLQDGSQVRAVYVMKFPQFTRNNNGASM- 131
Qy 128 NFEALAEATACROMGYSSKPTTRAVEIGDPQDLVVEITENSQELMRN--SSGPCLSGS 185
Db 132 ---KSRIESVLRLQNLNS-----GNLEINP---STISLTDQAANWLINCEGAPDLI-- 180
Qy 186 LVSLHCLACGKSLKTPRVVGEEASVDSWPQVSIQYDKQHVCGSILDHPHWTAAHCF 245
Db 181 -----TLSEQRILGCTEAEESGWPQVSLRNAHHCGLSLLNNWLLTAAHCF 229
Qy 246 RKHTDVFNKVRAGSKLGSFPSL--AVAKIIIEFNPMYPKNDIALMKLQFLPFTSGT 303

